

SEQUENCE LISTING

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Pan, Yang
- <120> NOVEL ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG, AND
STMST PROTEIN AND NUCLEIC ACID MOLECULES AND USES
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- <130> MNI-121CP
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- <150> PCT/US00/02125
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- <150> 09/448,076
<151> 1999-11-23
- <150> 09/276,400
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- <150> 60/117,580
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- <150> 09/014,195
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- <150> 09/086,892
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- <150> 09/561,810
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ata gaa gag agt ttc caa gaa atc aaa aga gcc atc caa gct aag gac      198
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gtc cac gct gct gcc att aaa tcc ctg gga gag ctc gac gtc ttt cta      534
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 Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
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 Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
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 Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His
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 Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr
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 gac atg cac cat ata gaa gag agt ttc caa gaa atc aaa aga gcc atc 144
 Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile
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 caa gct aag gac acc ttc cca aat gtc act atc ctg tcc aca ttg gag 192
 Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
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 act ctg cag atc att aag ccc tta gat gtg tgc tgc gtg acc aag aac 240
 Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn
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 ctc ctg gcg ttc tac gtg gac agg gtg ttc aag gat cat cag gag cca 288
 Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro
 85 90 95
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 Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
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 gac gtc ttt cta gcc tgg att aat aag aat cat gaa gta atg tcc tca 528
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 Asp Val Cys Cys Val Thr Lys Asn Leu Leu Ala Phe Tyr Val Asp Arg
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 Val Phe Lys Asp His Gln Glu Pro Asn Pro Lys Ile Leu Arg Lys Ile
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 Ser Ser Ile Ala Asn Ser Phe Leu Tyr Met Gln Lys Thr Leu Arg Gln
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Cys Tyr Leu Ala His Ser Leu Leu Lys Phe Tyr Leu Asn Thr Val Phe
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Lys Asn Tyr His Ser Lys Ile Ala Lys Phe Lys Val Leu Arg Ser Phe
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Ser Thr Leu Ala Asn Asn Phe Ile Val Ile Met Ser Gln Leu Gln Pro
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Ser Lys Asp Asn Ser Met Leu Pro Ile Ser Glu Ser Ala His Gln Arg
130 135 140

Phe Leu Leu Phe Arg Arg Thr Phe Lys Gln Leu Asp Thr Glu Val Ala
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Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val Phe Lys Asn
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Tyr His Asn Arg Thr Val Glu Val Arg Thr Leu Lys Ser Phe Ser Thr
100 105 110

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Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln Leu Gln Pro Ser Gln
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Glu Asn Glu Met Phe Ser Ile Arg Asp Ser Ala His Arg Arg Phe Leu
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 Met Arg Pro Val Ser Val Trp Gln Trp Ser
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ccc tgg ggg ctg ctg ctg tgc ctg ctg tgc agt tcg tgc ttg ggg tct 220
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cag	gag	ctc	tcc	ctc	tgg	aag	tgc	ccc	cac	aag	aac	atc	aca	gct	gag	1324
Gln	Glu	Leu	Ser	Leu	Trp	Lys	Cys	Pro	His	Lys	Asn	Ile	Thr	Ala	Glu	
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Gly	Leu	Ile	Cys	Gly	Asp	Asp	Trp	Gly	Thr	Leu	Glu	Ala	Met	Val	Ala	
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Ile	Cys	Ser	Glu	Thr	Ala	Ser	Asp	Leu	Leu	Leu	His	Ser	Ala	Leu	Val	
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Gln	Glu	Thr	Ala	Tyr	Ile	Glu	Asp	Arg	Pro	Leu	His	Met	Leu	Tyr	Cys	
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 Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly
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 225 230 235 240
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 Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro
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 Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile
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Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly
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His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro
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Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser
690 695 700

Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His
705 710 715 720

Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu
725 730 735

Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile
740 745 750

Ile

<210> 12
<211> 2262
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(2259)

<400> 12
atg cga cct gtc agt gtc tgg cag tgg agc ccc tgg ggg ctg ctg ctg 48
Met Arg Pro Val Ser Val Trp Gln Trp Ser Pro Trp Gly Leu Leu Leu
1 5 10 15

tgc ctg ctg tgc agt tcg tgc ttg ggg tct ccg tcc cct tcc acg ggc 96
Cys Leu Leu Cys Ser Ser Cys Leu Gly Ser Pro Ser Pro Ser Thr Gly
20 25 30

cct gag aag aag gcc ggg agc cag ggg ctt cgg ttc cgg ctg gct ggc 144
Pro Glu Lys Lys Ala Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala Gly
35 40 45

ttc ccc agg aag ccc tac gag ggc cgc gtg gag ata cag cga gct ggt 192
Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala Gly
50 55 60

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gaa tgg ggc acc atc tgc gat gat gac ttc acg ctg cag gct gcc cac	240
Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala His	
65 70 75 80	
atc ctc tgc cgg gag ctg ggc ttc aca gag gcc aca ggc tgg acc cac	288
Ile Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr His	
85 90 95	
agt gcc aaa tat ggc cct gga aca ggc cgc atc tgg ctg gac aac ttg	336
Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn Leu	
100 105 110	
agc tgc agt ggg acc gag cag agt gtg act gaa tgt gcc tcc cgg ggc	384
Ser Cys Ser Gly Thr Glu Gln Ser Val Thr Glu Cys Ala Ser Arg Gly	
115 120 125	
tgg ggg aac agt gac tgt acg cac gat gag gat gct ggg gtc atc tgc	432
Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile Cys	
130 135 140	
aaa gac cag cgc ctc cct ggc ttc tcg gac tcc aat gtc att gag gta	480
Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu Val	
145 150 155 160	
gag cat cac ctg caa gtg gag gag gtg cga att cga ccc gcc gtt ggg	528
Glu His His Leu Gln Val Glu Glu Val Arg Ile Arg Pro Ala Val Gly	
165 170 175	
tgg ggc aga cga ccc ctg ccc gtg acg gag ggg ctg gtg gaa gtc agg	576
Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val Arg	
180 185 190	
ctt cct gac ggc tgg tcg caa gtg tgc gac aaa ggc tgg agc gcc cac	624
Leu Pro Asp Gly Trp Ser Gln Val Cys Asp Lys Gly Trp Ser Ala His	
195 200 205	
aac agc cac gtg gtc tgc ggg atg ctg ggc ttc ccc agc gaa aag agg	672
Asn Ser His Val Val Cys Gly Met Leu Gly Phe Pro Ser Glu Lys Arg	
210 215 220	
gtc aac gcg gcc ttc tac agg ctg cta gcc caa cgg cag caa cac tcc	720
Val Asn Ala Ala Phe Tyr Arg Leu Leu Ala Gln Arg Gln Gln His Ser	
225 230 235 240	
ttt ggt ctg cat ggg gtg gcg tgc gtg ggc acg gag gcc cac ctc tcc	768
Phe Gly Leu His Gly Val Ala Cys Val Gly Thr Glu Ala His Leu Ser	
245 250 255	
ctc tgt tcc ctg gag ttc tat cgt gcc aat gac acc gcc agg tgc cct	816
Leu Cys Ser Leu Glu Phe Tyr Arg Ala Asn Asp Thr Ala Arg Cys Pro	
260 265 270	
ggg ggg ggc cct gca gtg gtg agc tgt gtg cca ggc cct gtc tac gcg	864
Gly Gly Gly Pro Ala Val Val Ser Cys Val Pro Gly Pro Val Tyr Ala	
275 280 285	
gca tcc agt ggc cag aag aag caa caa cag tcg aag cct cag ggg gag	912
Ala Ser Ser Gly Gln Lys Lys Gln Gln Gln Ser Lys Pro Gln Gly Glu	
290 295 300	

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gcc cgt gtc cgt cta aag ggc ggc gcc cac cct gga gag ggc cgg gta	960
Ala Arg Val Arg Leu Lys Gly Gly Ala His Pro Gly Glu Gly Arg Val	
305 310 315 320	
gaa gtc ctg aag gcc agc aca tgg ggc aca gtc tgt gac cgc aag tgg	1008
Glu Val Leu Lys Ala Ser Thr Trp Gly Thr Val Cys Asp Arg Lys Trp	
325 330 335	
gac ctg cat gca gcc agc gtg gtg tgt cgg gag ctg ggc ttc ggg agt	1056
Asp Leu His Ala Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser	
340 345 350	
gct cga gaa gct ctg agt ggc gct cgc atg ggg cag ggc atg ggt gct	1104
Ala Arg Glu Ala Leu Ser Gly Ala Arg Met Gly Gln Gly Met Gly Ala	
355 360 365	
atc cac ctg agt gaa gtt cgc tgc tct gga cag gag ctc tcc ctc tgg	1152
Ile His Leu Ser Glu Val Arg Cys Ser Gly Gln Glu Leu Ser Leu Trp	
370 375 380	
aag tgc ccc cac aag aac atc aca gct gag gat tgt tca cat agc cag	1200
Lys Cys Pro His Lys Asn Ile Thr Ala Glu Asp Cys Ser His Ser Gln	
385 390 395 400	
gat gcc ggg gtc cgg tgc aac cta cct tac act ggg gca gag acc agg	1248
Asp Ala Gly Val Arg Cys Asn Leu Pro Tyr Thr Gly Ala Glu Thr Arg	
405 410 415	
atc cga ctc agt ggg ggc cgc agc caa cat gag ggg cga gtc gag gtg	1296
Ile Arg Leu Ser Gly Gly Arg Ser Gln His Glu Gly Arg Val Glu Val	
420 425 430	
caa ata ggg gga cct ggg ccc ctt cgc tgg ggc ctc atc tgt ggg gat	1344
Gln Ile Gly Gly Pro Gly Pro Leu Arg Trp Gly Leu Ile Cys Gly Asp	
435 440 445	
gac tgg ggg acc ctg gag gcc atg gtg gcc tgt agg caa ctg ggt ctg	1392
Asp Trp Gly Thr Leu Glu Ala Met Val Ala Cys Arg Gln Leu Gly Leu	
450 455 460	
ggc tac gcc aac cac ggc ctg cag gag acc tgg tac tgg gac tct ggg	1440
Gly Tyr Ala Asn His Gly Leu Gln Glu Thr Trp Tyr Trp Asp Ser Gly	
465 470 475 480	
aat ata aca gag gtg gtg atg agt gga gtg cgc tgc aca ggg act gag	1488
Asn Ile Thr Glu Val Val Met Ser Gly Val Arg Cys Thr Gly Thr Glu	
485 490 495	
ctg tcc ctg gat cag tgt gcc cat cat ggc acc cac atc acc tgc aag	1536
Leu Ser Leu Asp Gln Cys Ala His His Gly Thr His Ile Thr Cys Lys	
500 505 510	
agg aca ggg acc cgc ttc act gct gga gtc atc tgt tct gag act gca	1584
Arg Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr Ala	
515 520 525	
tca gat ctg ttg ctg cac tca gca ctg gtg cag gag acc gcc tac atc	1632
Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr Ile	
530 535 540	

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gaa gac cgg ccc ctg cat atg ttg tac tgt gct gcg gaa gag aac tgc	1680
Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn Cys	
545 550 555 560	
ctg gcc agc tca gcc cgc tca gcc aac tgg ccc tat ggt cac cgg cgt	1728
Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg Arg	
565 570 575	
ctg ctc cga ttc tcc tcc cag atc cac aac ctg gga cga gct gac ttc	1776
Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp Phe	
580 585 590	
agg ccc aag gct ggg cgc cac tcc tgg gtg tgg cac gag tgc cat ggg	1824
Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His Gly	
595 600 605	
cat tac cac agc atg gac atc ttc act cac tat gat atc ctc acc cca	1872
His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr Pro	
610 615 620	
aat ggc acc aag gtg gct gag ggc cac aaa gct agt ttc tgt ctc gaa	1920
Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu Glu	
625 630 635 640	
gac act gag tgt cag gag gat gtc tcc aag cgg tat gag tgt gcc aac	1968
Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala Asn	
645 650 655	
ttt gga gag caa ggc atc act gtg ggt tgc tgg gat ctc tac cgg cat	2016
Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg His	
660 665 670	
gac att gac tgt cag tgg att gac atc acg gat gtg aag cca gga aac	2064
Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly Asn	
675 680 685	
tac att ctc cag gtt gtc atc aac cca aac ttt gaa gta gca gag agt	2112
Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu Ser	
690 695 700	
gac ttt acc aac aat gca atg aaa tgt aac tgc aaa tat gat gga cat	2160
Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly His	
705 710 715 720	
aga atc tgg gtg cac aac tgc cac att ggt gat gcc ttc agt gaa gag	2208
Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu Glu	
725 730 735	
gcc aac agg agg ttt gaa cgc tac cct ggc cag acc agc aac cag att	2256
Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln Ile	
740 745 750	
atc taa	2262
Ile	

<210> 13

<211> 38

<212> PRT

<213> Artificial Sequence

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<220>

<223> Description of Artificial Sequence: (SRRD)
consensus sequence

<220>

<223> Any occurrences of Xaa may be any amino acid

<400> 13

Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5					10					15	

Trp	Gly	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
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Xaa	Cys	Xaa	Xaa	Xaa	Gly
	35				

<210> 14

<211> 417

<212> PRT

<213> Homo sapiens

<400> 14

Met	Arg	Phe	Ala	Trp	Thr	Val	Leu	Leu	Leu	Gly	Pro	Leu	Gln	Leu	Cys
1				5					10					15	

Ala	Leu	Val	His	Cys	Ala	Pro	Pro	Ala	Ala	Gly	Gln	Gln	Gln	Pro	Pro
		20						25					30		

Arg	Glu	Pro	Pro	Ala	Ala	Pro	Gly	Ala	Trp	Arg	Gln	Gln	Ile	Gln	Trp
		35					40					45			

Glu	Asn	Asn	Gly	Gln	Val	Phe	Ser	Leu	Leu	Ser	Leu	Gly	Ser	Gln	Tyr
	50					55					60				

Gln	Pro	Gln	Arg	Arg	Arg	Asp	Pro	Gly	Ala	Ala	Val	Pro	Gly	Ala	Ala
	65				70					75					80

Asn	Ala	Ser	Ala	Gln	Gln	Pro	Arg	Thr	Pro	Ile	Leu	Leu	Ile	Arg	Asp
			85						90					95	

Asn	Arg	Thr	Ala	Ala	Gly	Arg	Thr	Arg	Thr	Ala	Gly	Ser	Ser	Gly	Val
		100						105					110		

Thr	Ala	Gly	Arg	Pro	Arg	Pro	Thr	Ala	Arg	His	Trp	Phe	Gln	Ala	Gly
		115					120					125			

Tyr	Ser	Thr	Ser	Arg	Ala	Arg	Glu	Ala	Gly	Pro	Ser	Arg	Ala	Glu	Asn
	130					135					140				

Gln	Thr	Ala	Pro	Gly	Glu	Val	Pro	Ala	Leu	Ser	Asn	Leu	Arg	Pro	Pro
	145				150					155					160

Ser	Arg	Val	Asp	Gly	Met	Val	Gly	Asp	Asp	Pro	Tyr	Asn	Pro	Tyr	Lys
				165					170					175	

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Tyr Ser Asp Asp Asn Pro Tyr Tyr Asn Tyr Tyr Asp Thr Tyr Glu Arg
 180 185 190
 Pro Arg Pro Gly Gly Arg Tyr Arg Pro Gly Tyr Gly Thr Gly Tyr Phe
 195 200 205
 Gln Tyr Gly Leu Pro Asp Leu Val Ala Asp Pro Tyr Tyr Ile Gln Ala
 210 215 220
 Ser Thr Tyr Val Gln Lys Met Ser Met Tyr Asn Leu Arg Cys Ala Ala
 225 230 235 240
 Glu Glu Asn Cys Leu Ala Ser Thr Ala Tyr Arg Ala Asp Val Arg Asp
 245 250 255
 Tyr Asp His Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln
 260 265 270
 Gly Thr Ser Asp Phe Leu Pro Ser Arg Pro Arg Tyr Ser Trp Glu Trp
 275 280 285
 His Ser Cys His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr
 290 295 300
 Asp Leu Leu Asp Ala Asn Thr Gln Arg Arg Val Ala Glu Gly His Lys
 305 310 315 320
 Ala Ser Phe Cys Leu Glu Asp Thr Ser Cys Asp Tyr Gly Tyr His Arg
 325 330 335
 Arg Phe Ala Cys Thr Ala His Thr Gln Gly Leu Ser Pro Gly Cys Tyr
 340 345 350
 Asp Thr Tyr Gly Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp
 355 360 365
 Val Lys Pro Gly Asn Tyr Ile Leu Lys Val Ser Val Asn Pro Ser Tyr
 370 375 380
 Leu Val Pro Glu Ser Asp Tyr Thr Asn Asn Val Val Arg Cys Asp Ile
 385 390 395 400
 Arg Tyr Thr Gly His His Ala Tyr Ala Ser Gly Cys Thr Ile Ser Pro
 405 410 415
 Tyr

<210> 15
 <211> 574
 <212> PRT
 <213> Homo sapiens

<400> 15
 Met Ala Leu Ala Arg Gly Ser Arg Gln Leu Gly Ala Leu Val Trp Gly
 1 5 10 15
 Ala Cys Leu Cys Val Leu Val His Gly Gln Gln Ala Gln Pro Gly Gln
 20 25 30

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Gly	Ser	Asp	Pro	Ala	Arg	Trp	Arg	Gln	Leu	Ile	Gln	Trp	Glu	Asn	Asn			
		35					40					45						
Gly	Gln	Val	Tyr	Ser	Leu	Leu	Asn	Ser	Gly	Ser	Glu	Tyr	Val	Pro	Ala			
	50					55					60							
Gly	Pro	Gln	Arg	Ser	Glu	Ser	Ser	Ser	Arg	Val	Leu	Leu	Ala	Gly	Ala			
	65				70					75					80			
Pro	Gln	Ala	Gln	Gln	Arg	Arg	Ser	His	Gly	Ser	Pro	Arg	Arg	Arg	Gln			
				85					90					95				
Ala	Pro	Ser	Leu	Pro	Leu	Pro	Gly	Arg	Val	Gly	Ser	Asp	Thr	Val	Arg			
			100					105					110					
Gly	Gln	Ala	Arg	His	Pro	Phe	Gly	Phe	Gly	Gln	Val	Pro	Asp	Asn	Trp			
		115					120					125						
Arg	Glu	Val	Ala	Val	Gly	Asp	Ser	Thr	Gly	Met	Ala	Leu	Ala	Arg	Thr			
	130					135					140							
Ser	Val	Ser	Gln	Gln	Arg	His	Gly	Gly	Ser	Ala	Ser	Ser	Val	Ser	Ala			
	145				150					155					160			
Ser	Ala	Phe	Ala	Ser	Thr	Tyr	Arg	Gln	Gln	Pro	Ser	Tyr	Pro	Gln	Gln			
				165					170					175				
Phe	Pro	Tyr	Pro	Gln	Ala	Pro	Phe	Val	Ser	Gln	Tyr	Glu	Asn	Tyr	Asp			
			180					185					190					
Pro	Ala	Ser	Arg	Thr	Tyr	Asp	Gln	Gly	Phe	Val	Tyr	Tyr	Arg	Pro	Ala			
		195				200						205						
Gly	Gly	Gly	Val	Gly	Ala	Gly	Ala	Ala	Ala	Val	Ala	Ser	Ala	Gly	Val			
	210					215					220							
Ile	Tyr	Pro	Tyr	Gln	Pro	Arg	Ala	Arg	Tyr	Glu	Glu	Tyr	Gly	Gly	Gly			
	225				230					235					240			
Glu	Glu	Leu	Pro	Glu	Tyr	Pro	Pro	Gln	Gly	Phe	Tyr	Pro	Ala	Pro	Glu			
				245					250					255				
Arg	Pro	Tyr	Val	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Asp	Gly	Leu	Asp	Arg			
			260					265					270					
Arg	Tyr	Ser	His	Ser	Leu	Tyr	Ser	Glu	Gly	Thr	Pro	Gly	Phe	Glu	Gln			
		275					280					285						
Ala	Tyr	Pro	Asp	Pro	Gly	Pro	Glu	Ala	Ala	Gln	Ala	His	Gly	Gly	Asp			
	290				295						300							
Pro	Arg	Leu	Gly	Trp	Tyr	Pro	Pro	Tyr	Ala	Asn	Pro	Pro	Pro	Glu	Ala			
	305				310					315				320				
Tyr	Gly	Pro	Pro	Arg	Ala	Leu	Glu	Pro	Pro	Tyr	Leu	Pro	Val	Arg	Ser			
				325					330					335				
Ser	Asp	Thr	Pro	Pro	Pro	Gly	Gly	Glu	Arg	Asn	Gly	Ala	Gln	Gln	Gly			
			340				345						350					

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Arg Leu Ser Val Gly Ser Val Tyr Arg Pro Asn Gln Asn Gly Arg Gly
 355 360 365
 Leu Pro Asp Leu Val Pro Asp Pro Asn Tyr Val Gln Ala Ser Thr Tyr
 370 375 380
 Val Gln Arg Ala His Leu Tyr Ser Leu Arg Cys Ala Ala Glu Glu Lys
 385 390 395 400
 Cys Leu Ala Ser Thr Ala Tyr Ala Pro Glu Ala Thr Asp Tyr Asp Val
 405 410 415
 Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln Gly Thr Ala
 420 425 430
 Asp Phe Leu Pro Asn Arg Pro Arg His Thr Trp Glu Trp His Ser Cys
 435 440 445
 His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr Asp Leu Leu
 450 455 460
 Asp Ala Ala Thr Gly Lys Lys Val Ala Glu Gly His Lys Ala Ser Phe
 465 470 475 480
 Cys Leu Glu Asp Ser Thr Cys Asp Phe Gly Asn Leu Lys Arg Tyr Ala
 485 490 495
 Cys Thr Ser His Thr Gln Gly Leu Ser Pro Gly Cys Tyr Asp Thr Tyr
 500 505 510
 Asn Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Gln Pro
 515 520 525
 Gly Asn Tyr Ile Leu Lys Val His Val Asn Pro Lys Tyr Ile Val Leu
 530 535 540
 Glu Ser Asp Phe Thr Asn Asn Val Val Arg Cys Asn Ile His Tyr Thr
 545 550 555 560
 Gly Arg Tyr Val Ser Ala Thr Asn Cys Lys Ile Val Gln Ser
 565 570

<210> 16

<211> 774

<212> PRT

<213> Homo sapiens

<400> 16

Met Glu Arg Pro Leu Cys Ser His Leu Cys Ser Cys Leu Ala Met Leu
 1 5 10 15
 Ala Leu Leu Ser Pro Leu Ser Leu Ala Gln Tyr Asp Ser Trp Pro His
 20 25 30
 Tyr Pro Glu Tyr Phe Gln Gln Pro Ala Pro Glu Tyr His Gln Pro Gln
 35 40 45

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Phe Gly Ser Ala Lys Glu Ala Val Thr Gly Ser Arg Leu Gly Gln Gly
 370 375 380
 Ile Gly Pro Ile His Leu Asn Glu Ile Gln Cys Thr Gly Asn Glu Lys
 385 390 395 400
 Ser Ile Ile Asp Cys Lys Phe Asn Ala Glu Ser Gln Gly Cys Asn His
 405 410 415
 Glu Glu Asp Ala Gly Val Arg Cys Asn Thr Pro Ala Met Gly Leu Gln
 420 425 430
 Lys Lys Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly Arg Val
 435 440 445
 Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met Val Cys
 450 455 460
 Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg Gln Leu
 465 470 475 480
 Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr Trp His
 485 490 495
 Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys Cys Ser
 500 505 510
 Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu Asp Val
 515 520 525
 Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala Cys Ser
 530 535 540
 Glu Thr Ala Pro Asp Leu Val Leu Asn Ala Glu Met Val Gln Gln Thr
 545 550 555 560
 Thr Tyr Leu Glu Asp Arg Pro Met Phe Met Leu Gln Cys Ala Met Glu
 565 570 575
 Glu Asn Cys Leu Ser Ala Ser Ala Ala Gln Thr Asp Pro Thr Thr Gly
 580 585 590
 Tyr Arg Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Asn Gly Gln
 595 600 605
 Ser Asp Phe Arg Pro Lys Asn Gly Arg His Ala Trp Ile Trp His Asp
 610 615 620
 Cys His Arg His Tyr His Ser Met Glu Val Phe Thr His Tyr Asp Leu
 625 630 635 640
 Leu Asn Leu Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe
 645 650 655
 Cys Leu Glu Asp Thr Glu Cys Glu Gly Asp Ile Gln Lys Asn Tyr Glu
 660 665 670
 Cys Ala Asn Phe Gly Asp Gln Gly Ile Thr Met Gly Cys Trp Asp Met
 675 680 685

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Tyr Arg His Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val Pro
690 695 700

Pro Gly Asp Tyr Leu Phe Gln Val Val Ile Asn Pro Asn Phe Glu Val
705 710 715 720

Ala Glu Ser Asp Tyr Ser Asn Asn Ile Met Lys Cys Arg Ser Arg Tyr
725 730 735

Asp Gly His Arg Ile Trp Met Tyr Asn Cys His Ile Gly Gly Ser Phe
740 745 750

Ser Glu Glu Thr Glu Lys Lys Phe Glu His Phe Ser Gly Leu Leu Asn
755 760 765

Asn Gln Leu Ser Pro Gln
770

<210> 17

<211> 754

<212> PRT

<213> Mus musculus

<400> 17

Met Arg Ala Val Ser Val Trp Tyr Cys Cys Pro Trp Gly Leu Leu Leu
1 5 10 15

Leu His Cys Leu Cys Ser Phe Ser Val Gly Ser Pro Ser Pro Ser Ile
20 25 30

Ser Pro Glu Lys Lys Val Gly Ser Gln Gly Leu Arg Phe Arg Leu Ala
35 40 45

Gly Phe Pro Arg Lys Pro Tyr Glu Gly Arg Val Glu Ile Gln Arg Ala
50 55 60

Gly Glu Trp Gly Thr Ile Cys Asp Asp Asp Phe Thr Leu Gln Ala Ala
65 70 75 80

His Val Leu Cys Arg Glu Leu Gly Phe Thr Glu Ala Thr Gly Trp Thr
85 90 95

His Ser Ala Lys Tyr Gly Pro Gly Thr Gly Arg Ile Trp Leu Asp Asn
100 105 110

Leu Ser Cys Arg Gly Thr Glu Gly Ser Val Thr Glu Cys Ala Ser Arg
115 120 125

Gly Trp Gly Asn Ser Asp Cys Thr His Asp Glu Asp Ala Gly Val Ile
130 135 140

Cys Lys Asp Gln Arg Leu Pro Gly Phe Ser Asp Ser Asn Val Ile Glu
145 150 155 160

Val Glu His Gln Leu Gln Val Glu Glu Val Arg Leu Arg Pro Ala Val
165 170 175

Glu Trp Gly Arg Arg Pro Leu Pro Val Thr Glu Gly Leu Val Glu Val
180 185 190

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Arg	Leu	Pro	Glu	Gly	Trp	Ser	Gln	Val	Cys	Asp	Lys	Gly	Trp	Ser	Ala			
		195					200					205						
His	Asn	Ser	His	Val	Val	Cys	Gly	Met	Leu	Gly	Phe	Pro	Gly	Glu	Lys			
	210					215					220							
Arg	Val	Asn	Met	Ala	Phe	Tyr	Arg	Met	Leu	Ala	Gln	Lys	Lys	Gln	His			
225					230					235					240			
Ser	Phe	Gly	Leu	His	Ser	Val	Ala	Cys	Val	Gly	Thr	Glu	Ala	His	Leu			
				245					250					255				
Ser	Leu	Cys	Ser	Leu	Glu	Phe	Tyr	Arg	Ala	Asn	Asp	Thr	Thr	Arg	Cys			
			260					265					270					
Ser	Gly	Gly	Asn	Pro	Ala	Val	Val	Ser	Cys	Val	Leu	Gly	Pro	Leu	Tyr			
		275					280					285						
Ala	Thr	Phe	Thr	Gly	Gln	Lys	Lys	Gln	Gln	His	Ser	Lys	Pro	Gln	Gly			
	290					295					300							
Glu	Ala	Arg	Val	Arg	Leu	Lys	Gly	Gly	Ala	His	Gln	Gly	Glu	Gly	Arg			
305					310					315					320			
Val	Glu	Val	Leu	Lys	Ala	Gly	Thr	Trp	Gly	Thr	Val	Cys	Asp	Arg	Lys			
				325					330					335				
Trp	Asp	Leu	Gln	Ala	Ala	Ser	Val	Val	Cys	Pro	Glu	Leu	Gly	Phe	Gly			
			340					345					350					
Thr	Ala	Arg	Glu	Ala	Leu	Ser	Gly	Ala	Arg	Met	Gly	Gln	Gly	Met	Gly			
		355					360					365						
Ala	Ile	His	Leu	Ser	Glu	Val	Arg	Cys	Ser	Gly	Gln	Glu	Pro	Ser	Leu			
	370					375					380							
Trp	Arg	Cys	Pro	Ser	Lys	Asn	Ile	Thr	Ala	Glu	Asp	Cys	Ser	His	Ser			
385					390					395					400			
Gln	Asp	Ala	Gly	Val	Arg	Cys	Asn	Leu	Pro	Tyr	Thr	Gly	Val	Glu	Thr			
				405					410					415				
Lys	Ile	Arg	Leu	Ser	Gly	Gly	Arg	Ser	Arg	Tyr	Glu	Gly	Arg	Val	Glu			
			420					425					430					
Val	Gln	Ile	Gly	Ile	Pro	Gly	His	Leu	Arg	Trp	Gly	Leu	Ile	Cys	Gly			
		435					440					445						
Asp	Asp	Trp	Gly	Thr	Leu	Glu	Ala	Met	Val	Ala	Cys	Arg	Gln	Leu	Gly			
	450					455					460							
Leu	Gly	Tyr	Ala	Asn	His	Gly	Leu	Gln	Glu	Thr	Trp	Tyr	Trp	Asp	Ser			
465					470					475					480			
Gly	Asn	Val	Thr	Glu	Val	Val	Met	Ser	Gly	Val	Arg	Cys	Thr	Gly	Ser			
				485					490					495				
Glu	Leu	Ser	Leu	Asn	Gln	Cys	Ala	His	His	Ser	Ser	His	Ile	Thr	Cys			
			500					505					510					

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Lys Lys Thr Gly Thr Arg Phe Thr Ala Gly Val Ile Cys Ser Glu Thr
 515 520 525
 Ala Ser Asp Leu Leu Leu His Ser Ala Leu Val Gln Glu Thr Ala Tyr
 530 535 540
 Ile Glu Asp Arg Pro Leu His Met Leu Tyr Cys Ala Ala Glu Glu Asn
 545 550 555 560
 Cys Leu Ala Ser Ser Ala Arg Ser Ala Asn Trp Pro Tyr Gly His Arg
 565 570 575
 Arg Leu Leu Arg Phe Ser Ser Gln Ile His Asn Leu Gly Arg Ala Asp
 580 585 590
 Phe Arg Pro Lys Ala Gly Arg His Ser Trp Val Trp His Glu Cys His
 595 600 605
 Gly His Tyr His Ser Met Asp Ile Phe Thr His Tyr Asp Ile Leu Thr
 610 615 620
 Pro Asn Gly Thr Lys Val Ala Glu Gly His Lys Ala Ser Phe Cys Leu
 625 630 635 640
 Glu Asp Thr Glu Cys Gln Glu Asp Val Ser Lys Arg Tyr Glu Cys Ala
 645 650 655
 Asn Phe Gly Glu Gln Gly Ile Thr Val Gly Cys Trp Asp Leu Tyr Arg
 660 665 670
 His Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp Val Lys Pro Gly
 675 680 685
 Asn Tyr Ile Leu Gln Val Val Ile Asn Pro Asn Phe Glu Val Ala Glu
 690 695 700
 Ser Asp Phe Thr Asn Asn Ala Met Lys Cys Asn Cys Lys Tyr Asp Gly
 705 710 715 720
 His Arg Ile Trp Val His Asn Cys His Ile Gly Asp Ala Phe Ser Glu
 725 730 735
 Glu Ala Asn Arg Arg Phe Glu Arg Tyr Pro Gly Gln Thr Ser Asn Gln
 740 745 750
 Ile Val

<210> 18

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

 <223> Description of Artificial Sequence: Copper-binding talon
 consensus sequence

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<400> 18

Trp Glu Trp His Ser Cys His Gln His Tyr His
 1 5 10

<210> 19

<211> 451

<212> PRT

<213> Homo sapiens

<400> 19

Met Glu Gln Trp Asp His Phe His Asn Gln Gln Glu Asp Thr Asp Ser
 1 5 10 15

Cys Ser Glu Ser Val Lys Phe Asp Ala Arg Ser Met Thr Ala Leu Leu
 20 25 30

Pro Pro Asn Pro Lys Asn Ser Pro Ser Leu Gln Glu Lys Leu Lys Ser
 35 40 45

Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu Val Phe Ala Val Leu
 50 55 60

Ile Pro Leu Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp Glu Thr
 65 70 75 80

Lys Asn Cys Ser Val Ser Ser Thr Asn Ala Asn Asp Ile Thr Gln Ser
 85 90 95

Leu Thr Gly Lys Gly Asn Asp Ser Glu Glu Glu Met Arg Phe Gln Glu
 100 105 110

Val Phe Met Glu His Met Ser Asn Met Glu Lys Arg Ile Gln His Ile
 115 120 125

Leu Asp Met Glu Ala Asn Leu Met Asp Thr Glu His Phe Gln Asn Phe
 130 135 140

Ser Met Thr Thr Asp Gln Arg Phe Asn Asp Ile Leu Leu Gln Leu Ser
 145 150 155 160

Thr Leu Phe Ser Ser Val Gln Gly His Gly Asn Ala Ile Asp Glu Ile
 165 170 175

Ser Lys Ser Leu Ile Ser Leu Asn Thr Thr Leu Leu Asp Leu Gln Leu
 180 185 190

Asn Ile Glu Asn Leu Asn Gly Lys Ile Gln Glu Asn Thr Phe Lys Gln
 195 200 205

Gln Glu Glu Ile Ser Lys Leu Glu Glu Arg Val Tyr Asn Val Ser Ala
 210 215 220

Glu Ile Met Ala Met Lys Glu Glu Gln Val His Leu Glu Gln Glu Ile
 225 230 235 240

Lys Gly Glu Val Lys Val Leu Asn Asn Ile Thr Asn Asp Leu Arg Leu
 245 250 255

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Lys Asp Trp Glu His Ser Gln Thr Leu Arg Asn Ile Thr Leu Ile Gln
260 265 270

Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Asp Arg Gly Pro Thr Gly
275 280 285

Glu Ser Gly Pro Arg Gly Phe Pro Gly Pro Ile Gly Pro Pro Gly Leu
290 295 300

Lys Gly Asp Arg Gly Ala Ile Gly Phe Pro Gly Ser Arg Gly Leu Pro
305 310 315 320

Gly Tyr Ala Gly Arg Pro Gly Asn Ser Gly Pro Lys Gly Gln Lys Gly
325 330 335

Glu Lys Gly Ser Gly Asn Thr Leu Thr Pro Phe Thr Lys Val Arg Leu
340 345 350

Val Gly Gly Ser Gly Pro His Glu Gly Arg Val Glu Ile Leu His Ser
355 360 365

Gly Gln Trp Gly Thr Ile Cys Asp Asp Arg Trp Glu Val Arg Val Gly
370 375 380

Gln Val Val Cys Arg Ser Leu Gly Tyr Pro Gly Val Gln Ala Val His
385 390 395 400

Lys Ala Ala His Phe Gly Gln Gly Thr Gly Pro Ile Trp Leu Asn Glu
405 410 415

Val Phe Cys Phe Gly Arg Glu Ser Ser Ile Glu Glu Cys Lys Ile Arg
420 425 430

Gln Trp Gly Thr Arg Ala Cys Ser His Ser Glu Asp Ala Gly Val Thr
435 440 445

Cys Thr Leu
450

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
gcttaccaag aaacccatgt cagc

24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

- 30 -

<400> 21
ggcagttagt caggtgctgc

20

<210> 22
<211> 981
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (107)..(748)

<400> 22
gaattcggca cgagggccgg cccccccgcg ccaccccagc ctcaaactgc agtccggcgc 60
cgcgggggcag gacaagggga aggaataaac acgttttggtg agagcc atg gca ctc 115
Met Ala Leu
1
aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc 163
Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe
5 10 15
cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg 211
Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg
20 25 30 35
cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag 259
Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln
40 45 50
tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg 307
Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly
55 60 65
gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac 355
Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp
70 75 80
tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac 403
Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn
85 90 95
cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg 451
Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly
100 105 110 115
gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa 499
Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln
120 125 130
gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc tac gaa cca 547
Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro
135 140 145
cac tgt acc agc aag gtg aac ctt gtg aag atc tcc tcc acc gtc tcc 595
His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser Thr Val Ser
150 155 160

- 31 -

agc cct cgg gac acg gcg ctg gct gcc gtc atc tgc agt gct ctg gcc 643
 Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala
 165 170 175

acg gtg ctg ctc gcc ctg ctc atc ctg tgt gtc atc tac tgc aag agg 691
 Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr Cys Lys Arg
 180 185 190 195

cag ttc atg gag aag aaa ccc agc tgt aag ctc cca tcc ctc tgt ctc 739
 Gln Phe Met Glu Lys Lys Pro Ser Cys Lys Leu Pro Ser Leu Cys Leu
 200 205 210

act gtg aag tgagcttggt agcattgtca cccaagagtt ctcaagacac 788
 Thr Val Lys

ctggctgaga cctaagacct ttagagcatc aacagctact tagaatacaa gatgcaggaa 848

aacgagcctc ttcaggaatc tcagggcctc ctagggatgc tggcaaggct gtgatgtctc 908

aaggctacca ggaaaaaata aaagttgtct ataccctaaa aaaaaaaaaa aaaaaaaaaa 968

aacatgcggc cgc 981

<210> 23

<211> 214

<212> PRT

<213> Mus musculus

<400> 23

Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
 1 5 10 15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
 20 25 30

Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
 35 40 45

Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 50 55 60

Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
 65 70 75 80

Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
 85 90 95

Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
 100 105 110

Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 115 120 125

Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
 130 135 140

Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser
 145 150 155 160

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Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser
 165 170 175

Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr
 180 185 190

Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Cys Lys Leu Pro Ser
 195 200 205

Leu Cys Leu Thr Val Lys
 210

<210> 24
 <211> 642
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(642)

<400> 24
 atg gca ctc aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc 48
 Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
 1 5 10 15

att ctc ttc cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga 96
 Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
 20 25 30

gat tgc agg cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc 144
 Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
 35 40 45

tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc 192
 Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 50 55 60

ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc 240
 Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
 65 70 75 80

aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg 288
 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
 85 90 95

ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct 336
 Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
 100 105 110

gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt 384
 Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 115 120 125

ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc 432
 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
 130 135 140

- 33 -

tac gaa cca cac tgt acc agc aag gtg aac ctt gtg aag atc tcc tcc	480
Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys Ile Ser Ser	
145 150 155 160	
acc gtc tcc agc cct cgg gac acg gcg ctg gct gcc gtc atc tgc agt	528
Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val Ile Cys Ser	
165 170 175	
gct ctg gcc acg gtg ctg ctc gcc ctg ctc atc ctg tgt gtc atc tac	576
Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys Val Ile Tyr	
180 185 190	
tgc aag agg cag ttc atg gag aag aaa ccc agc tgt aag ctc cca tcc	624
Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Cys Lys Leu Pro Ser	
195 200 205	
ctc tgt ctc act gtg aag	642
Leu Cys Leu Thr Val Lys	
210	
<210> 25	
<211> 555	
<212> DNA	
<213> Mus musculus	
<220>	
<221> CDS	
<222> (1)..(555)	
<400> 25	
gaa acc gga gat tgc agg cag cag gaa ttc aag gat cga tct gga aac	48
Glu Thr Gly Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn	
1 5 10 15	
tgt gtc ctc tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa	96
Cys Val Leu Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu	
20 25 30	
tgt ggc ttc ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg	144
Cys Gly Phe Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro	
35 40 45	
cac cgg ttc aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg	192
His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala	
50 55 60	
gac tgt gcg ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc	240
Asp Cys Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr	
65 70 75 80	
agt gat gct gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc	288
Ser Asp Ala Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr	
85 90 95	
aaa ctg gtt ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca	336
Lys Leu Val Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro	
100 105 110	

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cct cct ccc tac gaa cca cac tgt acc agc aag gtg aac ctt gtg aag 384
Pro Pro Pro Tyr Glu Pro His Cys Thr Ser Lys Val Asn Leu Val Lys
115 120 125

atc tcc tcc acc gtc tcc agc cct cgg gac acg gcg ctg gct gcc gtc 432
Ile Ser Ser Thr Val Ser Ser Pro Arg Asp Thr Ala Leu Ala Ala Val
130 135 140

atc tgc agt gct ctg gcc acg gtg ctg ctc gcc ctg ctc atc ctg tgt 480
Ile Cys Ser Ala Leu Ala Thr Val Leu Leu Ala Leu Leu Ile Leu Cys
145 150 155 160

gtc atc tac tgc aag agg cag ttc atg gag aag aaa ccc agc tgt aag 528
Val Ile Tyr Cys Lys Arg Gln Phe Met Glu Lys Lys Pro Ser Cys Lys
165 170 175

ctc cca tcc ctc tgt ctc act gtg aag 555
Leu Pro Ser Leu Cys Leu Thr Val Lys
180 185

<210> 26
<211> 655
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (110)..(559)

<400> 26
gaattcggca cgagggcggtt tggcgcggaa gtgctaccaa gctgcggaaa gcgtgagtct 60

ggagcacagc actggcgagt agcaggaata aacacgtttg gtgagagcc atg gca ctc 118
Met Ala Leu
1

aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc att ctc ttc 166
Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala Ile Leu Phe
5 10 15

cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga gat tgc agg 214
Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly Asp Cys Arg
20 25 30 35

cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc tgc aaa cag 262
Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu Cys Lys Gln
40 45 50

tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc ggc tat ggg 310
Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe Gly Tyr Gly
55 60 65

gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc aag gaa gac 358
Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe Lys Glu Asp
70 75 80

tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg ctg gtg aac 406
Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala Leu Val Asn
85 90 95

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cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct gtc tgc ggg 454
 Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala Val Cys Gly
 100 105 110 115

gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt ggt ttt caa 502
 Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val Gly Phe Gln
 120 125 130

gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc tac gaa cca 550
 Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro Tyr Glu Pro
 135 140 145

cac tgt gag tgatgtgcca agtggcagca gaccttttaa aaaaaaagaa 599
 His Cys Glu
 150

aaaaaaacaa acaaaaacaa aaaaaaaaaa aaaaaaaaaa aaattttccgc ggccgc 655

<210> 27
 <211> 150
 <212> PRT
 <213> Mus musculus

<400> 27
 Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
 1 5 10 15
 Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly
 20 25 30
 Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu
 35 40 45
 Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe
 50 55 60
 Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe
 65 70 75 80
 Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala
 85 90 95
 Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala
 100 105 110
 Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val
 115 120 125
 Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro
 130 135 140
 Tyr Glu Pro His Cys Glu
 145 150

- 36 -

<210> 28
 <211> 450
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(450)

<400> 28

atg gca ctc aag gtc cta cct cta cac agg acg gtg ctc ttc gct gcc	48
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala	
1 5 10 15	
att ctc ttc cta ctc cac ctg gca tgt aaa gtg agt tgc gaa acc gga	96
Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys Glu Thr Gly	
20 25 30	
gat tgc agg cag cag gaa ttc aag gat cga tct gga aac tgt gtc ctc	144
Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn Cys Val Leu	
35 40 45	
tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa tgt ggc ttc	192
Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu Cys Gly Phe	
50 55 60	
ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg cac cgg ttc	240
Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro His Arg Phe	
65 70 75 80	
aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg gac tgt gcg	288
Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala Asp Cys Ala	
85 90 95	
ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc agt gat gct	336
Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr Ser Asp Ala	
100 105 110	
gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc aaa ctg gtt	384
Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr Lys Leu Val	
115 120 125	
ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca cct cct ccc	432
Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro Pro Pro Pro	
130 135 140	
tac gaa cca cac tgt gag	450
Tyr Glu Pro His Cys Glu	
145 150	

<210> 29
 <211> 363
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(363)

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<400> 29

gaa acc gga gat tgc agg cag cag gaa ttc aag gat cga tct gga aac 48
 Glu Thr Gly Asp Cys Arg Gln Gln Glu Phe Lys Asp Arg Ser Gly Asn
 1 5 10 15

tgt gtc ctc tgc aaa cag tgc gga cct ggc atg gag ttg tcc aag gaa 96
 Cys Val Leu Cys Lys Gln Cys Gly Pro Gly Met Glu Leu Ser Lys Glu
 20 25 30

tgt ggc ttc ggc tat ggg gag gat gca cag tgt gtg ccc tgc agg ccg 144
 Cys Gly Phe Gly Tyr Gly Glu Asp Ala Gln Cys Val Pro Cys Arg Pro
 35 40 45

cac cgg ttc aag gaa gac tgg ggt ttc cag aag tgt aag cca tgt gcg 192
 His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys Pro Cys Ala
 50 55 60

gac tgt gcg ctg gtg aac cgc ttt cag agg gcc aac tgc tca cac acc 240
 Asp Cys Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys Ser His Thr
 65 70 75 80

agt gat gct gtc tgc ggg gac tgc ctg cca gga ttt tac cgg aag acc 288
 Ser Asp Ala Val Cys Gly Asp Cys Leu Pro Gly Phe Tyr Arg Lys Thr
 85 90 95

aaa ctg gtt ggt ttt caa gac atg gag tgt gtg ccc tgc gga gac cca 336
 Lys Leu Val Gly Phe Gln Asp Met Glu Cys Val Pro Cys Gly Asp Pro
 100 105 110

cct cct ccc tac gaa cca cac tgt gag 363
 Pro Pro Pro Tyr Glu Pro His Cys Glu
 115 120

<210> 30

<211> 272

<212> PRT

<213> Mus musculus

<400> 30

Met Tyr Val Trp Val Gln Gln Pro Thr Ala Leu Leu Leu Leu Ala Leu
 1 5 10 15

Thr Leu Gly Val Thr Ala Arg Arg Leu Asn Cys Val Lys His Thr Tyr
 20 25 30

Pro Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met
 35 40 45

Val Ser Arg Cys Asp His Thr Arg Asp Thr Leu Cys His Pro Cys Glu
 50 55 60

Thr Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys
 65 70 75 80

Thr Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr
 85 90 95

Pro Thr Gln Asp Thr Val Cys Arg Cys Arg Pro Gly Thr Gln Pro Arg
 100 105 110

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Gln Asp Ser Gly Tyr Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro
 115 120 125
 Gly His Phe Ser Pro Gly Asn Asn Gln Ala Cys Lys Pro Trp Thr Asn
 130 135 140
 Cys Thr Leu Ser Gly Lys Gln Thr Arg His Pro Ala Ser Asp Ser Leu
 145 150 155 160
 Asp Ala Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu
 165 170 175
 Thr Gln Arg Pro Thr Phe Arg Pro Thr Thr Val Gln Ser Thr Thr Val
 180 185 190
 Trp Pro Arg Thr Ser Glu Leu Pro Ser Pro Pro Thr Leu Val Thr Pro
 195 200 205
 Glu Gly Pro Ala Phe Ala Val Leu Leu Gly Leu Gly Leu Gly Leu Leu
 210 215 220
 Ala Pro Leu Thr Val Leu Leu Ala Leu Tyr Leu Leu Arg Lys Ala Trp
 225 230 235 240
 Arg Leu Pro Asn Thr Pro Lys Pro Cys Trp Gly Asn Ser Phe Arg Thr
 245 250 255
 Pro Ile Gln Glu Glu His Thr Asp Ala His Phe Thr Leu Ala Lys Ile
 260 265 270

<210> 31
 <211> 1344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (273)..(1022)

<400> 31
 gaattcggaa cgaggggaac ctaattctcc tgaggctgag ggaggggtgga gggctctcaag 60
 gcaacgctgg cccacgacg gagtgccagg agcactaaca gtacccttag cttgctttcc 120
 tcctccctcc tttttatttt caagttcctt tttattttctc cttgcgtaac aaccttcttc 180
 ctttctgcac cactgcccgt acccttacct gccccgccac ctcttgcta cccactctt 240
 gaaaccacag ctgttggcag ggtccccagc tc atg cca gcc tca tct cct ttc 293
 Met Pro Ala Ser Ser Pro Phe
 1 5
 ttg cta gcc ccc aaa ggg cct cca ggc aac atg ggg ggc cca gtc aga 341
 Leu Leu Ala Pro Lys Gly Pro Pro Gly Asn Met Gly Gly Pro Val Arg
 10 15 20

- 39 -

gag ccg gca ctc tca gtt gcc ctc tgg ttg agt tgg ggg gca gct ctg	389
Glu Pro Ala Leu Ser Val Ala Leu Trp Leu Ser Trp Gly Ala Ala Leu	
25 30 35	
ggg gcc gtg gct tgt gcc atg gct ctg ctg acc caa caa aca gag ctg	437
Gly Ala Val Ala Cys Ala Met Ala Leu Leu Thr Gln Gln Thr Glu Leu	
40 45 50 55	
cag agc ctc agg aga gag gtg agc cgg ctg cag ggg aca gga ggc ccc	485
Gln Ser Leu Arg Arg Glu Val Ser Arg Leu Gln Gly Thr Gly Gly Pro	
60 65 70	
tcc cag aat ggg gaa ggg tat ccc tgg cag agt ctc ccg gag cag agt	533
Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser	
75 80 85	
tcc gat gcc ctg gaa gcc tgg gag aat ggg gag aga tcc cgg aaa agg	581
Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg	
90 95 100	
aga gca gtg ctc acc caa aaa cag aag aag cag cac tct gtc ctg cac	629
Arg Ala Val Leu Thr Gln Lys Gln Lys Lys Gln His Ser Val Leu His	
105 110 115	
ctg gtt ccc att aac gcc acc tcc aag gat gac tcc gat gtg aca gag	677
Leu Val Pro Ile Asn Ala Thr Ser Lys Asp Asp Ser Asp Val Thr Glu	
120 125 130 135	
gtg atg tgg caa cca gct ctt agg cgt ggg aga ggc cta cag gcc caa	725
Val Met Trp Gln Pro Ala Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln	
140 145 150	
gga tat ggt gtc cga atc cag gat gct gga gtt tat ctg ctg tat agc	773
Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser	
155 160 165	
cag gtc ctg ttt caa gac gtg act ttc acc atg ggt cag gtg gtg tct	821
Gln Val Leu Phe Gln Asp Val Thr Phe Thr Met Gly Gln Val Val Ser	
170 175 180	
cga gaa ggc caa gga agg cag gag act cta ttc cga tgt ata aga agt	869
Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser	
185 190 195	
atg ccc tcc cac ccg gac cgg gcc tac aac agc tgc tat agc gca ggt	917
Met Pro Ser His Pro Asp Arg Ala Tyr Asn Ser Cys Tyr Ser Ala Gly	
200 205 210 215	
gtc ttc cat tta cac caa ggg gat att ctg agt gtc ata att ccc cgg	965
Val Phe His Leu His Gln Gly Asp Ile Leu Ser Val Ile Ile Pro Arg	
220 225 230	
gca agg gcg aaa ctt aac ctc tct cca cat gga acc ttc ctg ggg ttt	1013
Ala Arg Ala Lys Leu Asn Leu Ser Pro His Gly Thr Phe Leu Gly Phe	
235 240 245	
gtg aaa ctg tgattgtgtt ataaaaagtg gctcccagct tggaagacca	1062
Val Lys Leu	
250	

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gggtgggtac atactggaga cagccaagag ctgagtatat aaaggagagg gaatgtgcag 1122
 gaacagagge atcttcctgg gtttggctcc ccgttcctca cttttccctt ttcattccca 1182
 ccccctagac tttgatttta cggatatctt gcttctgttc cccatggagc tccgaattct 1242
 tgogtgtgtg tagatgaggg gcgggggacg ggcgccaggc attgttcaga cctggtcggg 1302
 gccactgga agcatccaga acagcaccac catctagcgg cc 1344

<210> 32
 <211> 250
 <212> PRT
 <213> Homo sapiens

<400> 32
 Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
 1 5 10 15
 Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
 20 25 30
 Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
 35 40 45
 Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg
 50 55 60
 Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp
 65 70 75 80
 Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn
 85 90 95
 Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys
 100 105 110
 Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys
 115 120 125
 Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg
 130 135 140
 Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala
 145 150 155 160
 Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe
 165 170 175
 Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr
 180 185 190
 Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr
 195 200 205
 Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile
 210 215 220

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Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
 225 230 235 240

His Gly Thr Phe Leu Gly Phe Val Lys Leu
 245 250

<210> 33
 <211> 754
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(750)

<400> 33
 atg cca gcc tca tct cct ttc ttg cta gcc ccc aaa ggg cct cca ggc 48
 Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
 1 5 10 15
 aac atg ggg ggc cca gtc aga gag ccg gca ctc tca gtt gcc ctc tgg 96
 Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
 20 25 30
 ttg agt tgg ggg gca gct ctg ggg gcc gtg gct tgt gcc atg gct ctg 144
 Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
 35 40 45
 ctg acc caa caa aca gag ctg cag agc ctc agg aga gag gtg agc cgg 192
 Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg
 50 55 60
 ctg cag ggg aca gga ggc ccc tcc cag aat ggg gaa ggg tat ccc tgg 240
 Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp
 65 70 75 80
 cag agt ctc ccg gag cag agt tcc gat gcc ctg gaa gcc tgg gag aat 288
 Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn
 85 90 95
 ggg gag aga tcc cgg aaa agg aga gca gtg ctc acc caa aaa cag aag 336
 Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys
 100 105 110
 aag cag cac tct gtc ctg cac ctg gtt ccc att aac gcc acc tcc aag 384
 Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys
 115 120 125
 gat gac tcc gat gtg aca gag gtg atg tgg caa cca gct ctt agg cgt 432
 Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg
 130 135 140
 ggg aga ggc cta cag gcc caa gga tat ggt gtc cga atc cag gat gct 480
 Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala
 145 150 155 160
 gga gtt tat ctg ctg tat agc cag gtc ctg ttt caa gac gtg act ttc 528
 Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe
 165 170 175

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acc atg ggt cag gtg gtg tct cga gaa ggc caa gga agg cag gag act 576
 Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr
 180 185 190

cta ttc cga tgt ata aga agt atg ccc tcc cac ccg gac cgg gcc tac 624
 Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr
 195 200 205

aac agc tgc tat agc gca ggt gtc ttc cat tta cac caa ggg gat att 672
 Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile
 210 215 220

ctg agt gtc ata att ccc cgg gca agg gcg aaa ctt aac ctc tct cca 720
 Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro
 225 230 235 240

cat gga acc ttc ctg ggg ttt gtg aaa ctg tgat 754
 His Gly Thr Phe Leu Gly Phe Val Lys Leu
 245 250

<210> 34
 <211> 17
 <212> PRT
 <213> Homo sapiens

<400> 34
 Val Arg Ile Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu
 1 5 10 15

Phe

<210> 35
 <211> 49
 <212> PRT
 <213> Homo sapiens

<400> 35
 Met Pro Ala Ser Ser Pro Phe Leu Leu Ala Pro Lys Gly Pro Pro Gly
 1 5 10 15

Asn Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp
 20 25 30

Leu Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu
 35 40 45

Leu

<210> 36
 <211> 603
 <212> DNA
 <213> Homo sapiens

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<210> 37
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 37
 Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg Leu
 1 5 10 15
 Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln
 20 25 30
 Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly
 35 40 45
 Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys
 50 55 60
 Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp
 65 70 75 80
 Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly
 85 90 95
 Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly
 100 105 110
 Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr
 115 120 125
 Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu
 130 135 140
 Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn
 145 150 155 160
 Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu
 165 170 175
 Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His
 180 185 190
 Gly Thr Phe Leu Gly Phe Val Lys Leu
 195 200

<210> 38
 <211> 699
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(699)

<400> 38
 atg ggg ggc cca gtc aga gag ccg gca ctc tca gtt gcc ctc tgg ttg 48
 Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp Leu
 1 5 10 15

- 45 -

agt tgg ggg gca gct ctg ggg gcc gtg gct tgt gcc atg gct ctg ctg	96
Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu Leu	
20 25 30	
acc caa caa aca gag ctg cag agc ctc agg aga gag gtg agc cgg ctg	144
Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg Leu	
35 40 45	
cag ggg aca gga ggc ccc tcc cag aat ggg gaa ggg tat ccc tgg cag	192
Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln	
50 55 60	
agt ctc ccg gag cag agt tcc gat gcc ctg gaa gcc tgg gag aat ggg	240
Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly	
65 70 75 80	
gag aga tcc cgg aaa agg aga gca gtg ctc acc caa aaa cag aag aag	288
Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys	
85 90 95	
cag cac tct gtc ctg cac ctg gtt ccc att aac gcc acc tcc aag gat	336
Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp	
100 105 110	
gac tcc gat gtg aca gag gtg atg tgg caa cca gct ctt agg cgt ggg	384
Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly	
115 120 125	
aga ggc cta cag gcc caa gga tat ggt gtc cga atc cag gat gct gga	432
Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly	
130 135 140	
gtt tat ctg ctg tat agc cag gtc ctg ttt caa gac gtg act ttc acc	480
Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr	
145 150 155 160	
atg ggt cag gtg gtg tct cga gaa ggc caa gga agg cag gag act cta	528
Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu	
165 170 175	
ttc cga tgt ata aga agt atg ccc tcc cac ccg gac cgg gcc tac aac	576
Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn	
180 185 190	
agc tgc tat agc gca ggt gtc ttc cat tta cac caa ggg gat att ctg	624
Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu	
195 200 205	
agt gtc ata att ccc cgg gca agg gcg aaa ctt aac ctc tct cca cat	672
Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His	
210 215 220	
gga acc ttc ctg ggg ttt gtg aaa ctg	699
Gly Thr Phe Leu Gly Phe Val Lys Leu	
225 230	

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<210> 39
 <211> 233
 <212> PRT
 <213> Homo sapiens

<400> 39
 Met Gly Gly Pro Val Arg Glu Pro Ala Leu Ser Val Ala Leu Trp Leu
 1 5 10 15
 Ser Trp Gly Ala Ala Leu Gly Ala Val Ala Cys Ala Met Ala Leu Leu
 20 25 30
 Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu Val Ser Arg Leu
 35 40 45
 Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly Tyr Pro Trp Gln
 50 55 60
 Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala Trp Glu Asn Gly
 65 70 75 80
 Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln Lys Gln Lys Lys
 85 90 95
 Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala Thr Ser Lys Asp
 100 105 110
 Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala Leu Arg Arg Gly
 115 120 125
 Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile Gln Asp Ala Gly
 130 135 140
 Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp Val Thr Phe Thr
 145 150 155 160
 Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg Gln Glu Thr Leu
 165 170 175
 Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp Arg Ala Tyr Asn
 180 185 190
 Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln Gly Asp Ile Leu
 195 200 205
 Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn Leu Ser Pro His
 210 215 220
 Gly Thr Phe Leu Gly Phe Val Lys Leu
 225 230

<210> 40
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(615)

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<400> 40

atg gct ctg ctg acc caa caa aca gag ctg cag agc ctc agg aga gag	48
Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu	
1 5 10 15	
gtg agc cgg ctg cag ggg aca gga ggc ccc tcc cag aat ggg gaa ggg	96
Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly	
20 25 30	
tat ccc tgg cag agt ctc ccg gag cag agt tcc gat gcc ctg gaa gcc	144
Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala	
35 40 45	
tgg gag aat ggg gag aga tcc cgg aaa agg aga gca gtg ctc acc caa	192
Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln	
50 55 60	
aaa cag aag aag cag cac tct gtc ctg cac ctg gtt ccc att aac gcc	240
Lys Gln Lys Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala	
65 70 75 80	
acc tcc aag gat gac tcc gat gtg aca gag gtg atg tgg caa cca gct	288
Thr Ser Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala	
85 90 95	
ctt agg cgt ggg aga ggc cta cag gcc caa gga tat ggt gtc cga atc	336
Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile	
100 105 110	
cag gat gct gga gtt tat ctg ctg tat agc cag gtc ctg ttt caa gac	384
Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp	
115 120 125	
gtg act ttc acc atg ggt cag gtg gtg tct cga gaa ggc caa gga agg	432
Val Thr Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg	
130 135 140	
cag gag act cta ttc cga tgt ata aga agt atg ccc tcc cac ccg gac	480
Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp	
145 150 155 160	
cgg gcc tac aac agc tgc tat agc gca ggt gtc ttc cat tta cac caa	528
Arg Ala Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln	
165 170 175	
ggg gat att ctg agt gtc ata att ccc cgg gca agg gcg aaa ctt aac	576
Gly Asp Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn	
180 185 190	
ctc tct cca cat gga acc ttc ctg ggg ttt gtg aaa ctg	615
Leu Ser Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu	
195 200 205	

<210> 41

<211> 205

<212> PRT

<213> Homo sapiens

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<400> 41

Met Ala Leu Leu Thr Gln Gln Thr Glu Leu Gln Ser Leu Arg Arg Glu
 1 5 10 15

Val Ser Arg Leu Gln Gly Thr Gly Gly Pro Ser Gln Asn Gly Glu Gly
 20 25 30

Tyr Pro Trp Gln Ser Leu Pro Glu Gln Ser Ser Asp Ala Leu Glu Ala
 35 40 45

Trp Glu Asn Gly Glu Arg Ser Arg Lys Arg Arg Ala Val Leu Thr Gln
 50 55 60

Lys Gln Lys Lys Gln His Ser Val Leu His Leu Val Pro Ile Asn Ala
 65 70 75 80

Thr Ser Lys Asp Asp Ser Asp Val Thr Glu Val Met Trp Gln Pro Ala
 85 90 95

Leu Arg Arg Gly Arg Gly Leu Gln Ala Gln Gly Tyr Gly Val Arg Ile
 100 105 110

Gln Asp Ala Gly Val Tyr Leu Leu Tyr Ser Gln Val Leu Phe Gln Asp
 115 120 125

Val Thr Phe Thr Met Gly Gln Val Val Ser Arg Glu Gly Gln Gly Arg
 130 135 140

Gln Glu Thr Leu Phe Arg Cys Ile Arg Ser Met Pro Ser His Pro Asp
 145 150 155 160

Arg Ala Tyr Asn Ser Cys Tyr Ser Ala Gly Val Phe His Leu His Gln
 165 170 175

Gly Asp Ile Leu Ser Val Ile Ile Pro Arg Ala Arg Ala Lys Leu Asn
 180 185 190

Leu Ser Pro His Gly Thr Phe Leu Gly Phe Val Lys Leu
 195 200 205

<210> 42

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
 sequence

<220>

<223> Xaas at position 2, 4-6, 12, 13 and 16 may be any
 amino acid

<220>

<223> Any 2 of the Xaas at positions 4-6 may be absent,
 intended to equal a range of 1-3;

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<220>

<223> Any 1 of the Xaas at positions 12-13 may be absent,
intended to equal a range of 1-2;

<400> 42

Val	Xaa	Ile	Xaa	Xaa	Xaa	Gly	Val	Tyr	Leu	Leu	Xaa	Xaa	Glu	Val	Xaa
1				5					10					15	

Phe

<210> 43

<211> 233

<212> PRT

<213> Homo sapiens

<400> 43

Met	Ser	Thr	Glu	Ser	Met	Ile	Arg	Asp	Val	Glu	Leu	Ala	Glu	Glu	Ala
1				5					10					15	

Leu	Pro	Lys	Lys	Thr	Gly	Gly	Pro	Gln	Gly	Ser	Arg	Arg	Cys	Leu	Phe
			20					25					30		

Leu	Ser	Leu	Phe	Ser	Phe	Leu	Ile	Val	Ala	Gly	Ala	Thr	Thr	Leu	Phe
		35					40					45			

Cys	Leu	Leu	His	Phe	Gly	Val	Ile	Gly	Pro	Gln	Arg	Glu	Glu	Phe	Pro
	50					55					60				

Arg	Asp	Leu	Ser	Leu	Ile	Ser	Pro	Leu	Ala	Gln	Ala	Val	Arg	Ser	Ser
65					70					75					80

Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn	Pro
				85					90					95	

Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu
		100						105					110		

Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser
		115					120					125			

Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly
	130					135					140				

Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile	Ala
145					150					155					160

Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	Ala	Ile	Lys	Ser	Pro
				165					170					175	

Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp	Tyr	Glu
			180					185					190		

Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Lys	Gly	Asp	Arg	Leu
		195					200					205			

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Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
 210 215 220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
 225 230

<210> 44
 <211> 249
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Ala Ala Arg Arg Ser Gln Arg Arg Arg Gly Arg Arg Gly Glu Pro
 1 5 10 15

Gly Thr Ala Leu Leu Val Pro Leu Ala Leu Gly Leu Gly Leu Ala Leu
 20 25 30

Ala Cys Leu Gly Leu Leu Leu Ala Val Val Ser Leu Gly Ser Arg Ala
 35 40 45

Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu Glu Leu Val Ala Glu Glu
 50 55 60

Asp Gln Asp Pro Ser Glu Leu Asn Pro Gln Thr Glu Glu Ser Gln Asp
 65 70 75 80

Pro Ala Pro Phe Leu Asn Arg Leu Val Arg Pro Arg Arg Ser Ala Pro
 85 90 95

Lys Gly Arg Lys Thr Arg Ala Arg Arg Ala Ile Ala Ala His Tyr Glu
 100 105 110

Val His Pro Arg Pro Gly Gln Asp Gly Ala Gln Ala Gly Val Asp Gly
 115 120 125

Thr Val Ser Gly Trp Glu Glu Ala Arg Ile Asn Ser Ser Ser Pro Leu
 130 135 140

Arg Tyr Asn Arg Gln Ile Gly Glu Phe Ile Val Thr Arg Ala Gly Leu
 145 150 155 160

Tyr Tyr Leu Tyr Cys Gln Val His Phe Asp Glu Gly Lys Ala Val Tyr
 165 170 175

Leu Lys Leu Asp Leu Leu Val Asp Gly Val Leu Ala Leu Arg Cys Leu
 180 185 190

Glu Glu Phe Ser Ala Thr Ala Ala Ser Ser Leu Gly Pro Gln Leu Arg
 195 200 205

Leu Cys Gln Val Ser Gly Leu Leu Ala Leu Arg Pro Gly Ser Ser Leu
 210 215 220

Arg Ile Arg Thr Leu Pro Trp Ala His Leu Lys Ala Ala Pro Phe Leu
 225 230 235 240

Thr Tyr Phe Gly Leu Phe Gln Val His
 245

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<210> 45
 <211> 1119
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (140)..(871)

<400> 45

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gtcgacccac gcgtccggca ggatgtttgc agtgtcgcgc ccagggctct gagactgagc 60
ctgccatcca ctgcacgcc tttctttcag ggcttttcgg ctgttggtta cactgatgtg 120
acccccctcc ctttttggga atg atg ggg atc ttt ttg gtg tat gtt gga ttt 172
          Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe
                1                5                10

gtt ttc ttt tcc gtt tta tat gta caa caa ggg ctt tct tct caa gca 220
Val Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala
                15                20                25

aaa ttt acc gag ttt ccg cgg aac gtg acg gcg acc gag ggg cag aat 268
Lys Phe Thr Glu Phe Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn
                30                35                40

gtg gag atg tcc tgc gcc ttc cag agc ggc tcc gcc tcg gtg tat ctg 316
Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu
                45                50                55

gag atc caa tgg tgg ttc ctg cgg ggg ccg gag gac ctg gat ccc ggg 364
Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly
                60                65                70                75

gcc gag ggg gcc ggc gcg cag gtg gag ctc ttg ccc gac aga gac ccg 412
Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro
                80                85                90

gac agc gac ggg acc aag atc agc aca gtg aaa gtc caa ggc aat gac 460
Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp
                95                100                105

atc tcc cac aag ctt cag att tcc aaa gtg agg aaa aag gat gaa ggc 508
Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly
                110                115                120

tta tat gag tgc agg gtg act gat gcc aac tac ggg gag ctt cag gaa 556
Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu
                125                130                135

cac aag gcc cag gcc tat ctg aaa gtc aat gcc aac agc cat gcc cgc 604
His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg
                140                145                150                155

aga atg cag gcc ttc gaa gcc tcg ccc atg tgg ctg cag gat atg aag 652
Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys
                160                165                170

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ccc cgc aag aac gtc tcc gca gcc atc ccc agc agc atc cat ggc tct 700
Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser
175 180 185

gcc aac caa cga acg cac tcc acc tcc agc cct caa gtg gta gcc aaa 748
Ala Asn Gln Arg Thr His Ser Thr Ser Ser Pro Gln Val Val Ala Lys
190 195 200

atc ccc aaa caa agt cca caa tca ggt atg gaa acc cat ttc gag cct 796
Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro
205 210 215

ttt att tta cca ctc aca aac gct cca cag aaa ggt cag tcg tat aga 844
Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg
220 225 230 235

gta gac aga ttt atg aat ggt gat ttt taaaatcgga gacctagttc 891
Val Asp Arg Phe Met Asn Gly Asp Phe
240

agtgcaagtg attatgagag gtgagcactg agcctgcacc aattcactca gagctcaaag 951
catgtgggtg caccocgtca gtccoctagt ggtgcttcat ttccagggca tctgagagct 1011
ggactctggt ttttatacctt tctgtattta cacattataa gaacaataaa tcatgtaatg 1071
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<213> Homo sapiens

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20 25 30
Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys
35 40 45
Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp
50 55 60
Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly Ala Glu Gly Ala Gly
65 70 75 80
Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Ser Asp Gly Thr
85 90 95
Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu
100 105 110
Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg
115 120 125

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- 53 -

Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu His Lys Ala Gln Ala
130 135 140

Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gln Ala Phe
145 150 155 160

Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys Pro Arg Lys Asn Val
165 170 175

Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser Ala Asn Gln Arg Thr
180 185 190

His Ser Thr Ser Ser Pro Gln Val Val Ala Lys Ile Pro Lys Gln Ser
195 200 205

Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro Phe Ile Leu Pro Leu
210 215 220

Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg Val Asp Arg Phe Met
225 230 235 240

Asn Gly Asp Phe

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<211> 735

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<213> Homo sapiens

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<222> (1)..(732)

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1 5 10 15

tta tat gta caa caa ggg ctt tct tct caa gca aaa ttt acc gag ttt 96
Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala Lys Phe Thr Glu Phe
20 25 30

ccg cgg aac gtg acg gcg acc gag ggg cag aat gtg gag atg tcc tgc 144
Pro Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys
35 40 45

gcc ttc cag agc ggc tcc gcc tcg gtg tat ctg gag atc caa tgg tgg 192
Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp
50 55 60

ttc ctg cgg ggg ccg gag gac ctg gat ccc ggg gcc gag ggg gcc ggc 240
Phe Leu Arg Gly Pro Glu Asp Leu Asp Pro Gly Ala Glu Gly Ala Gly
65 70 75 80

gcg cag gtg gag ctc ttg ccc gac aga gac ccg gac agc gac ggg acc 288
Ala Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Ser Asp Gly Thr
85 90 95

- 54 -

aag atc agc aca gtg aaa gtc caa ggc aat gac atc tcc cac aag ctt 336
Lys Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu
100 105 110

cag att tcc aaa gtg agg aaa aag gat gaa ggc tta tat gag tgc agg 384
Gln Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg
115 120 125

gtg act gat gcc aac tac ggg gag ctt cag gaa cac aag gcc cag gcc 432
Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu His Lys Ala Gln Ala
130 135 140

tat ctg aaa gtc aat gcc aac agc cat gcc cgc aga atg cag gcc ttc 480
Tyr Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gln Ala Phe
145 150 155 160

gaa gcc tcg ccc atg tgg ctg cag gat atg aag ccc cgc aag aac gtc 528
Glu Ala Ser Pro Met Trp Leu Gln Asp Met Lys Pro Arg Lys Asn Val
165 170 175

tcc gca gcc atc ccc agc agc atc cat ggc tct gcc aac caa cga acg 576
Ser Ala Ala Ile Pro Ser Ser Ile His Gly Ser Ala Asn Gln Arg Thr
180 185 190

cac tcc acc tcc agc cct caa gtg gta gcc aaa atc ccc aaa caa agt 624
His Ser Thr Ser Ser Pro Gln Val Val Ala Lys Ile Pro Lys Gln Ser
195 200 205

cca caa tca ggt atg gaa acc cat ttc gag cct ttt att tta cca ctc 672
Pro Gln Ser Gly Met Glu Thr His Phe Glu Pro Phe Ile Leu Pro Leu
210 215 220

aca aac gct cca cag aaa ggt cag tcg tat aga gta gac aga ttt atg 720
Thr Asn Ala Pro Gln Lys Gly Gln Ser Tyr Arg Val Asp Arg Phe Met
225 230 235 240

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<211> 660

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<213> Homo sapiens

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cag aat gtg gag atg tcc tgc gcc ttc cag agc ggc tcc gcc tcg gtg 96
Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val
20 25 30

- 55 -

tat ctg gag atc caa tgg tgg ttc ctg cgg ggg ccg gag gac ctg gat	144
Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp	
35 40 45	
ccc ggg gcc gag ggg gcc ggc gcg cag gtg gag ctc ttg ccc gac aga	192
Pro Gly Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg	
50 55 60	
gac ccg gac agc gac ggg acc aag atc agc aca gtg aaa gtc caa ggc	240
Asp Pro Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly	
65 70 75 80	
aat gac atc tcc cac aag ctt cag att tcc aaa gtg agg aaa aag gat	288
Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp	
85 90 95	
gaa ggc tta tat gag tgc agg gtg act gat gcc aac tac ggg gag ctt	336
Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu	
100 105 110	
cag gaa cac aag gcc cag gcc tat ctg aaa gtc aat gcc aac agc cat	384
Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His	
115 120 125	
gcc cgc aga atg cag gcc ttc gaa gcc tcg ccc atg tgg ctg cag gat	432
Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp	
130 135 140	
atg aag ccc cgc aag aac gtc tcc gca gcc atc ccc agc agc atc cat	480
Met Lys Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His	
145 150 155 160	
ggc tct gcc aac caa cga acg cac tcc acc tcc agc cct caa gtg gta	528
Gly Ser Ala Asn Gln Arg Thr His Ser Thr Ser Ser Pro Gln Val Val	
165 170 175	
gcc aaa atc ccc aaa caa agt cca caa tca ggt atg gaa acc cat ttc	576
Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe	
180 185 190	
gag cct ttt att tta cca ctc aca aac gct cca cag aaa ggt cag tcg	624
Glu Pro Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser	
195 200 205	
tat aga gta gac aga ttt atg aat ggt gat ttt taa	660
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20 25 30	

- 56 -

Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Asp
35 40 45

Pro Gly Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp Arg
50 55 60

Asp Pro Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly
65 70 75 80

Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp
85 90 95

Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu
100 105 110

Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His
115 120 125

Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp
130 135 140

Met Lys Pro Arg Lys Asn Val Ser Ala Ala Ile Pro Ser Ser Ile His
145 150 155 160

Gly Ser Ala Asn Gln Arg Thr His Ser Thr Ser Ser Pro Gln Val Val
165 170 175

Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Gly Met Glu Thr His Phe
180 185 190

Glu Pro Phe Ile Leu Pro Leu Thr Asn Ala Pro Gln Lys Gly Gln Ser
195 200 205

Tyr Arg Val Asp Arg Phe Met Asn Gly Asp Phe
210 215

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<213> Mus musculus

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<222> (268)..(1020)

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gtccaagcta ctctttgcta tgagcggcag catgcgtgca gtatcgcgcc ccaggctctg 180
agagcagcct gcggacacgc ttgcctatct gtcttttttag gttttggggc tctgggctac 240
acggatgtgc cccactccct tggcatg atg ggg atc ttt ttg gcg tct gtt gga 294
Met Gly Ile Phe Leu Ala Ser Val Gly

- 57 -

ttt atg ttc ttt tcc gtg tta tat gta caa caa ggg ctt tct tct caa	342
Phe Met Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln	
10 15 20 25	
gca aaa ttt acc gag ttg ccg aga aat gtg act gct acc gaa ggg caa	390
Ala Lys Phe Thr Glu Leu Pro Arg Asn Val Thr Ala Thr Glu Gly Gln	
30 35 40	
aat gtg gag atg tcc tgt gct ttc caa agc ggc tct gct tca gtg tac	438
Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val Tyr	
45 50 55	
ctg gag atc cag tgg tgg ttc ctt cgg ggg cca gag gac ctg gag caa	486
Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu Gln	
60 65 70	
ggc acg gag gct gca ggc tcg cag gtg gag ctc tta ccc gac aga gac	534
Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg Asp	
75 80 85	
ccg gac aac gat ggg acc aag att agt aca gtg aaa gtc caa ggc aat	582
Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly Asn	
90 95 100 105	
gat atc tcc cac aag ctt cag ata tcc aaa gtg aga aaa aag gat gaa	630
Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp Glu	
110 115 120	
ggt tta tac gag tgc agg gtg act gac gct aac tac ggg gag ctt cag	678
Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu Gln	
125 130 135	
gaa cac aag gcc cag gcc tat ctg aaa gtc aat gcc aac agc cat gct	726
Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His Ala	
140 145 150	
cgg agg atg cag gcc ttt gaa gcc tca cct atg tgg ctg caa gac acg	774
Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp Thr	
155 160 165	
aag cct cga aag aac gca tca tcg gtg gtt ccc agc agc gtc cac aac	822
Lys Pro Arg Lys Asn Ala Ser Ser Val Val Pro Ser Ser Val His Asn	
170 175 180 185	
tct gcc aac caa cga atg cac tcc acc tcc agc cct caa gcg gta gcc	870
Ser Ala Asn Gln Arg Met His Ser Thr Ser Ser Pro Gln Ala Val Ala	
190 195 200	
aaa atc ccc aag caa agt cca caa tca gca aag agc aaa tcg cct gta	918
Lys Ile Pro Lys Gln Ser Pro Gln Ser Ala Lys Ser Lys Ser Pro Val	
205 210 215	
aaa tct acg gag cgg aca gca aag ttg acc cta tac tcc aag cac cat	966
Lys Ser Thr Glu Arg Thr Ala Lys Leu Thr Leu Tyr Ser Lys His His	
220 225 230	
tct gca ccc ctg tac tct agt tat cta cac aag gag cat cag ctt ccg	1014
Ser Ala Pro Leu Tyr Ser Ser Tyr Leu His Lys Glu His Gln Leu Pro	
235 240 245	

- 58 -

gaa gca taagtgaaga cactgtcaca cgctttattg ataatatattt ctttgggaag 1070
 Glu Ala
 250

ttgctgatct tttattttcaa gagaattaat gggaagagat aggacatttt ccaattacaa 1130
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 aatgtctact aattaaaaat taaaatgtga ttgttggtg aatacaatat gcaaatgact 2270
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 atggtaaatc tttccttgcc atttttcttc tttcatttga ttcatattt cattctaattg 2750

- 59 -

aagaaaataa aggtttaatt atgatacttt attaacatac aaatgtattt tcttttctaag 2810
ttaaatatct gaaagttgta taaaatgatg gtagagaaat attactcatt cggtttcttt 2870
gagctttaag aatcccatatc attgcagtat atattagaat actgatttaa catcaaactg 2930
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atatgctagt tttggaagaa tgctcattag attcattgta tcagtgtcca aaataataaa 3110
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<211> 251

<212> PRT

<213> Mus musculus

<400> 51

Met Gly Ile Phe Leu Ala Ser Val Gly Phe Met Phe Phe Ser Val Leu
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20 25 30

Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys Ala
35 40 45

Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp Phe
50 55 60

Leu Arg Gly Pro Glu Asp Leu Glu Gln Gly Thr Glu Ala Ala Gly Ser
65 70 75 80

Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Asn Asp Gly Thr Lys
85 90 95

Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu Gln
100 105 110

Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg Val
115 120 125

Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu His Lys Ala Gln Ala Tyr
130 135 140

Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gln Ala Phe Glu
145 150 155 160

Ala Ser Pro Met Trp Leu Gln Asp Thr Lys Pro Arg Lys Asn Ala Ser
165 170 175

Ser Val Val Pro Ser Ser Val His Asn Ser Ala Asn Gln Arg Met His
180 185 190

- 60 -

Ser Thr Ser Ser Pro Gln Ala Val Ala Lys Ile Pro Lys Gln Ser Pro
 195 200 205

Gln Ser Ala Lys Ser Lys Ser Pro Val Lys Ser Thr Glu Arg Thr Ala
 210 215 220

Lys Leu Thr Leu Tyr Ser Lys His His Ser Ala Pro Leu Tyr Ser Ser
 225 230 235 240

Tyr Leu His Lys Glu His Gln Leu Pro Glu Ala
 245 250

<210> 52
 <211> 756
 <212> DNA
 <213> Mus musculus

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 1 5 10 15

tat gta caa caa ggg ctt tct tct caa gca aaa ttt acc gag ttg ccg 96
 Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala Lys Phe Thr Glu Leu Pro
 20 25 30

aga aat gtg act gct acc gaa ggg caa aat gtg gag atg tcc tgt gct 144
 Arg Asn Val Thr Ala Thr Glu Gly Gln Asn Val Glu Met Ser Cys Ala
 35 40 45

ttc caa agc ggc tct gct tca gtg tac ctg gag atc cag tgg tgg ttc 192
 Phe Gln Ser Gly Ser Ala Ser Val Tyr Leu Glu Ile Gln Trp Trp Phe
 50 55 60

ctt cgg ggg cca gag gac ctg gag caa ggc acg gag gct gca ggc tcg 240
 Leu Arg Gly Pro Glu Asp Leu Glu Gln Gly Thr Glu Ala Ala Gly Ser
 65 70 75 80

cag gtg gag ctc tta ccc gac aga gac ccg gac aac gat ggg acc aag 288
 Gln Val Glu Leu Leu Pro Asp Arg Asp Pro Asp Asn Asp Gly Thr Lys
 85 90 95

att agt aca gtg aaa gtc caa ggc aat gat atc tcc cac aag ctt cag 336
 Ile Ser Thr Val Lys Val Gln Gly Asn Asp Ile Ser His Lys Leu Gln
 100 105 110

ata tcc aaa gtg aga aaa aag gat gaa ggt tta tac gag tgc agg gtg 384
 Ile Ser Lys Val Arg Lys Lys Asp Glu Gly Leu Tyr Glu Cys Arg Val
 115 120 125

act gac gct aac tac ggg gag ctt cag gaa cac aag gcc cag gcc tat 432
 Thr Asp Ala Asn Tyr Gly Glu Leu Gln Glu His Lys Ala Gln Ala Tyr
 130 135 140

- 61 -

ctg aaa gtc aat gcc aac agc cat gct cgg agg atg cag gcc ttt gaa 480
 Leu Lys Val Asn Ala Asn Ser His Ala Arg Arg Met Gln Ala Phe Glu
 145 150 155 160

gcc tca cct atg tgg ctg caa gac acg aag cct cga aag aac gca tca 528
 Ala Ser Pro Met Trp Leu Gln Asp Thr Lys Pro Arg Lys Asn Ala Ser
 165 170 175

tcg gtg gtt ccc agc agc gtc cac aac tct gcc aac caa cga atg cac 576
 Ser Val Val Pro Ser Ser Val His Asn Ser Ala Asn Gln Arg Met His
 180 185 190

tcc acc tcc agc cct caa gcg gta gcc aaa atc ccc aag caa agt cca 624
 Ser Thr Ser Ser Pro Gln Ala Val Ala Lys Ile Pro Lys Gln Ser Pro
 195 200 205

caa tca gca aag agc aaa tcg cct gta aaa tct acg gag cgg aca gca 672
 Gln Ser Ala Lys Ser Lys Ser Pro Val Lys Ser Thr Glu Arg Thr Ala
 210 215 220

aag ttg acc cta tac tcc aag cac cat tct gca ccc ctg tac tct agt 720
 Lys Leu Thr Leu Tyr Ser Lys His His Ser Ala Pro Leu Tyr Ser Ser
 225 230 235 240

tat cta cac aag gag cat cag ctt ccg gaa gca taa 756
 Tyr Leu His Lys Glu His Gln Leu Pro Glu Ala
 245 250

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 <211> 684
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(681)

<400> 53

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caa aat gtg gag atg tcc tgt gct ttc caa agc ggc tct gct tca gtg 96
 Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser Val
 20 25 30

tac ctg gag atc cag tgg tgg ttc ctt cgg ggg cca gag gac ctg gag 144
 Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu Glu
 35 40 45

caa ggc acg gag gct gca ggc tcg cag gtg gag ctc tta ccc gac aga 192
 Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp Arg
 50 55 60

gac ccg gac aac gat ggg acc aag att agt aca gtg aaa gtc caa ggc 240
 Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly
 65 70 75 80

- 62 -

aat	gat	atc	tcc	cac	aag	ctt	cag	ata	tcc	aaa	gtg	aga	aaa	aag	gat	288
Asn	Asp	Ile	Ser	His	Lys	Leu	Gln	Ile	Ser	Lys	Val	Arg	Lys	Lys	Asp	
				85					90						95	

gaa	ggt	tta	tac	gag	tgc	agg	gtg	act	gac	gct	aac	tac	ggg	gag	ctt	336
Glu	Gly	Leu	Tyr	Glu	Cys	Arg	Val	Thr	Asp	Ala	Asn	Tyr	Gly	Glu	Leu	
			100					105					110			

cag	gaa	cac	aag	gcc	cag	gcc	tat	ctg	aaa	gtc	aat	gcc	aac	agc	cat	384
Gln	Glu	His	Lys	Ala	Gln	Ala	Tyr	Leu	Lys	Val	Asn	Ala	Asn	Ser	His	
		115					120					125				

gct	cgg	agg	atg	cag	gcc	ttt	gaa	gcc	tca	cct	atg	tgg	ctg	caa	gac	432
Ala	Arg	Arg	Met	Gln	Ala	Phe	Glu	Ala	Ser	Pro	Met	Trp	Leu	Gln	Asp	
	130					135					140					

acg	aag	cct	cga	aag	aac	gca	tca	tcg	gtg	gtt	ccc	agc	agc	gtc	cac	480
Thr	Lys	Pro	Arg	Lys	Asn	Ala	Ser	Ser	Val	Val	Pro	Ser	Ser	Val	His	
145					150					155					160	

aac	tct	gcc	aac	caa	cga	atg	cac	tcc	acc	tcc	agc	cct	caa	gcg	gta	528
Asn	Ser	Ala	Asn	Gln	Arg	Met	His	Ser	Thr	Ser	Ser	Pro	Gln	Ala	Val	
				165					170					175		

gcc	aaa	atc	ccc	aag	caa	agt	cca	caa	tca	gca	aag	agc	aaa	tcg	cct	576
Ala	Lys	Ile	Pro	Lys	Gln	Ser	Pro	Gln	Ser	Ala	Lys	Ser	Lys	Ser	Pro	
			180					185					190			

gta	aaa	tct	acg	gag	cgg	aca	gca	aag	ttg	acc	cta	tac	tcc	aag	cac	624
Val	Lys	Ser	Thr	Glu	Arg	Thr	Ala	Lys	Leu	Thr	Leu	Tyr	Ser	Lys	His	
		195					200					205				

cat	tct	gca	ccc	ctg	tac	tct	agt	tat	cta	cac	aag	gag	cat	cag	ctt	672
His	Ser	Ala	Pro	Leu	Tyr	Ser	Ser	Tyr	Leu	His	Lys	Glu	His	Gln	Leu	
	210					215					220					

ccg	gaa	gca	taa													684
Pro	Glu	Ala														
225																

<210> 54
 <211> 227
 <212> PRT
 <213> Mus musculus

<400> 54																
Gln	Ala	Lys	Phe	Thr	Glu	Leu	Pro	Arg	Asn	Val	Thr	Ala	Thr	Glu	Gly	
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Gln	Asn	Val	Glu	Met	Ser	Cys	Ala	Phe	Gln	Ser	Gly	Ser	Ala	Ser	Val	
			20					25					30			
Tyr	Leu	Glu	Ile	Gln	Trp	Trp	Phe	Leu	Arg	Gly	Pro	Glu	Asp	Leu	Glu	
		35					40					45				
Gln	Gly	Thr	Glu	Ala	Ala	Gly	Ser	Gln	Val	Glu	Leu	Leu	Pro	Asp	Arg	
	50					55					60					

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Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln Gly
 65 70 75 80

Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys Asp
 85 90 95

Glu Gly Leu Tyr Glu Cys Arg Val Thr Asp Ala Asn Tyr Gly Glu Leu
 100 105 110

Gln Glu His Lys Ala Gln Ala Tyr Leu Lys Val Asn Ala Asn Ser His
 115 120 125

Ala Arg Arg Met Gln Ala Phe Glu Ala Ser Pro Met Trp Leu Gln Asp
 130 135 140

Thr Lys Pro Arg Lys Asn Ala Ser Ser Val Val Pro Ser Ser Val His
 145 150 155 160

Asn Ser Ala Asn Gln Arg Met His Ser Thr Ser Ser Pro Gln Ala Val
 165 170 175

Ala Lys Ile Pro Lys Gln Ser Pro Gln Ser Ala Lys Ser Lys Ser Pro
 180 185 190

Val Lys Ser Thr Glu Arg Thr Ala Lys Leu Thr Leu Tyr Ser Lys His
 195 200 205

His Ser Ala Pro Leu Tyr Ser Ser Tyr Leu His Lys Glu His Gln Leu
 210 215 220

Pro Glu Ala
 225

<210> 55
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 55
 Gly Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser
 1 5 10 15

Val Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu
 20 25 30

Asp Pro Gly Ala Glu Gly Ala Gly Ala Gln Val Glu Leu Leu Pro Asp
 35 40 45

Arg Asp Pro Asp Ser Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln
 50 55 60

Gly Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys
 65 70 75 80

Asp Glu Gly Leu Tyr Glu Cys Arg Val
 85

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<210> 56
 <211> 89
 <212> PRT
 <213> Mus musculus

<400> 56
 Gly Gln Asn Val Glu Met Ser Cys Ala Phe Gln Ser Gly Ser Ala Ser
 1 5 10 15
 Val Tyr Leu Glu Ile Gln Trp Trp Phe Leu Arg Gly Pro Glu Asp Leu
 20 25 30
 Glu Gln Gly Thr Glu Ala Ala Gly Ser Gln Val Glu Leu Leu Pro Asp
 35 40 45
 Arg Asp Pro Asp Asn Asp Gly Thr Lys Ile Ser Thr Val Lys Val Gln
 50 55 60
 Gly Asn Asp Ile Ser His Lys Leu Gln Ile Ser Lys Val Arg Lys Lys
 65 70 75 80
 Asp Glu Gly Leu Tyr Glu Cys Arg Val
 85

<210> 57
 <211> 47
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Consensus
 sequence

<400> 57
 Gly Gln Ser Val Thr Leu Thr Cys Met Val Ser Phe His Pro Pro Asp
 1 5 10 15
 Tyr Thr Ile Trp Trp Tyr Arg Asn Gly Gln Pro Ile Thr Leu Thr Ile
 20 25 30
 Asn Ser Trp Gln Tyr Glu Asp Ser Glu Thr Tyr Trp Cys Met Val
 35 40 45

<210> 58
 <211> 2852
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (160)..(2178)

<400> 58
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 ggacccagga cccctcggg cccgacccgc caggaaagac tgaggccgcg gcctgccccg 120

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cccggtcccc	tgcgcccgcg	ccgcctccccg	ggacagaag	atg	tgc	tcc	agg	gtc									174
				Met	Cys	Ser	Arg	Val									
				1				5									
cct	ctg	ctg	ctg	ccg	ctg	ctc	ctg	cta	ctg	gcc	ctg	ggg	cct	ggg	gtg		222
Pro	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Gly	Pro	Gly	Val		
				10					15					20			
cag	ggc	tgc	cca	tcc	ggc	tgc	cag	tgc	agc	cag	cca	cag	aca	gtc	ttc		270
Gln	Gly	Cys	Pro	Ser	Gly	Cys	Gln	Cys	Ser	Gln	Pro	Gln	Thr	Val	Phe		
			25					30					35				
tgc	act	gcc	cgc	cag	ggg	acc	acg	gtg	ccc	cga	gac	gtg	cca	ccc	gac		318
Cys	Thr	Ala	Arg	Gln	Gly	Thr	Thr	Val	Pro	Arg	Asp	Val	Pro	Pro	Asp		
		40					45					50					
acg	gtg	ggg	ctg	tac	gtc	ttt	gag	aac	ggc	atc	acc	atg	ctc	gac	gca		366
Thr	Val	Gly	Leu	Tyr	Val	Phe	Glu	Asn	Gly	Ile	Thr	Met	Leu	Asp	Ala		
	55					60					65						
ggc	agc	ttt	gcc	ggc	ctg	ccg	ggc	ctg	cag	ctc	ctg	gac	ctg	tca	cag		414
Gly	Ser	Phe	Ala	Gly	Leu	Pro	Gly	Leu	Gln	Leu	Leu	Asp	Leu	Ser	Gln		
70					75					80					85		
aac	cag	atc	gcc	agc	ctg	ccc	agc	ggg	gtc	ttc	cag	cca	ctc	gcc	aac		462
Asn	Gln	Ile	Ala	Ser	Leu	Pro	Ser	Gly	Val	Phe	Gln	Pro	Leu	Ala	Asn		
				90					95					100			
ctc	agc	aac	ctg	gac	ctg	acg	gcc	aac	agg	ctg	cat	gaa	atc	acc	aat		510
Leu	Ser	Asn	Leu	Asp	Leu	Thr	Ala	Asn	Arg	Leu	His	Glu	Ile	Thr	Asn		
			105					110					115				
gag	acc	ttc	cgt	ggc	ctg	cgg	cgc	ctc	gag	cgc	ctc	tac	ctg	ggc	aag		558
Glu	Thr	Phe	Arg	Gly	Leu	Arg	Arg	Leu	Glu	Arg	Leu	Tyr	Leu	Gly	Lys		
		120					125					130					
aac	cgc	atc	cgc	cac	atc	cag	cct	ggt	gcc	ttc	gac	acg	ctc	gac	cgc		606
Asn	Arg	Ile	Arg	His	Ile	Gln	Pro	Gly	Ala	Phe	Asp	Thr	Leu	Asp	Arg		
		135				140					145						
ctc	ctg	gag	ctc	aag	ctg	cag	gac	aac	gag	ctg	cgg	gca	ctg	ccc	ccg		654
Leu	Leu	Glu	Leu	Lys	Leu	Gln	Asp	Asn	Glu	Leu	Arg	Ala	Leu	Pro	Pro		
150					155				160						165		
ctg	cgc	ctg	ccc	cgc	ctg	ctg	ctg	ctg	gac	ctc	agc	cac	aac	agc	ctc		702
Leu	Arg	Leu	Pro	Arg	Leu	Leu	Leu	Leu	Asp	Leu	Ser	His	Asn	Ser	Leu		
				170					175					180			
ctg	gcc	ctg	gag	ccc	ggc	atc	ctg	gac	act	gcc	aac	gtg	gag	gcg	ctg		750
Leu	Ala	Leu	Glu	Pro	Gly	Ile	Leu	Asp	Thr	Ala	Asn	Val	Glu	Ala	Leu		
			185					190					195				
cgg	ctg	gct	ggt	ctg	ggg	ctg	cag	cag	ctg	gac	gag	ggg	ctc	ttc	agc		798
Arg	Leu	Ala	Gly	Leu	Gly	Leu	Gln	Gln	Leu	Asp	Glu	Gly	Leu	Phe	Ser		
		200					205					210					
cgc	ttg	cgc	aac	ctc	cac	gac	ctg	gat	gtg	tcc	gac	aac	cag	ctg	gag		846
Arg	Leu	Arg	Asn	Leu	His	Asp	Leu	Asp	Val	Ser	Asp	Asn	Gln	Leu	Glu		
		215				220					225						

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cga gtg cca cct gtg atc cga ggc ctc cgg ggc ctg acg cgc ctg cgg	894
Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly Leu Thr Arg Leu Arg	
230 235 240 245	
ctg gcc ggc aac acc cgc att gcc cag ctg cgg ccc gag gac ctg gcc	942
Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu Arg Pro Glu Asp Leu Ala	
250 255 260	
ggc ctg gct gcc ctg cag gag ctg gat gtg agc aac cta agc ctg cag	990
Gly Leu Ala Ala Leu Gln Glu Leu Asp Val Ser Asn Leu Ser Leu Gln	
265 270 275	
gcc ctg cct gcc gac ctc tcg ggc ctc ttc ccc cgc ctg cgg ctg ctg	1038
Ala Leu Pro Gly Asp Leu Ser Gly Leu Phe Pro Arg Leu Arg Leu Leu	
280 285 290	
gca gct gcc cgc aac ccc ttc aac tgc gtg tgc ccc ctg agc tgg ttt	1086
Ala Ala Ala Arg Asn Pro Phe Asn Cys Val Cys Pro Leu Ser Trp Phe	
295 300 305	
ggc ccc tgg gtg cgc gag agc cac gtc aca ctg gcc agc cct gag gag	1134
Gly Pro Trp Val Arg Glu Ser His Val Thr Leu Ala Ser Pro Glu Glu	
310 315 320 325	
acg cgc tgc cac ttc ccg ccc aag aac gct ggc cgg ctg ctc ctg gag	1182
Thr Arg Cys His Phe Pro Pro Lys Asn Ala Gly Arg Leu Leu Leu Glu	
330 335 340	
ctt gac tac gcc gac ttt ggc tgc cca gcc acc acc acc aca gcc aca	1230
Leu Asp Tyr Ala Asp Phe Gly Cys Pro Ala Thr Thr Thr Thr Ala Thr	
345 350 355	
gtg ccc acc acg agg ccc gtg gtg cgg gag ccc aca gcc ttg tct tct	1278
Val Pro Thr Thr Arg Pro Val Val Arg Glu Pro Thr Ala Leu Ser Ser	
360 365 370	
agc ttg gct cct acc tgg ctt agc ccc aca gcg ccg gcc act gag gcc	1326
Ser Leu Ala Pro Thr Trp Leu Ser Pro Thr Ala Pro Ala Thr Glu Ala	
375 380 385	
ccc agc ccg ccc tcc act gcc cca ccg act gta ggg cct gtc ccc cag	1374
Pro Ser Pro Pro Ser Thr Ala Pro Pro Thr Val Gly Pro Val Pro Gln	
390 395 400 405	
ccc cag gac tgc cca ccg tcc acc tgc ctc aat ggg ggc aca tgc cac	1422
Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn Gly Gly Thr Cys His	
410 415 420	
ctg ggg aca cgg cac cac ctg gcg tgc ttg tgc ccc gaa ggc ttc acg	1470
Leu Gly Thr Arg His His Leu Ala Cys Leu Cys Pro Glu Gly Phe Thr	
425 430 435	
ggc ctg tac tgt gag agc cag atg ggg cag ggg aca cgg ccc agc cct	1518
Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg Pro Ser Pro	
440 445 450	
aca cca gtc acg ccg agg cca cca cgg tcc ctg acc ctg ggc atc gag	1566
Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr Leu Gly Ile Glu	
455 460 465	

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ctccgcaacg tgcagtcctt gggcacggcg ggccttgcca tgtgctggta acgcatgcct 2488
 gggccttgct gggctctccc actccaggcg gaccctgggg gccagtgaag gaagctcccg 2548
 gaaagagcag agggagagcg ggtaggcggc tgtgtgactc tagtcttggc cccaggaagc 2608
 gaaggaacaa aagaaactgg aaaggaagat gctttaggaa catgttttgc ttttttaaaa 2668
 tatatatata ttataagag atcctttccc atttattctg ggaagatggt tttcaaactc 2728
 agagacaagg actttggttt ttgtaagaca aacgatgata tgaaggcctt ttgtaagaaa 2788
 aaataaaaga tgaagtgtga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaagggcgg 2848
 ccgc 2852

<210> 59
 <211> 673
 <212> PRT
 <213> Homo sapiens

<400> 59
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 Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys Ser Gln
 20 25 30
 Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr Val Pro Arg
 35 40 45
 Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe Glu Asn Gly Ile
 50 55 60
 Thr Met Leu Asp Ala Gly Ser Phe Ala Gly Leu Pro Gly Leu Gln Leu
 65 70 75 80
 Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser Leu Pro Ser Gly Val Phe
 85 90 95
 Gln Pro Leu Ala Asn Leu Ser Asn Leu Asp Leu Thr Ala Asn Arg Leu
 100 105 110
 His Glu Ile Thr Asn Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu Arg
 115 120 125
 Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile Gln Pro Gly Ala Phe
 130 135 140
 Asp Thr Leu Asp Arg Leu Leu Glu Leu Lys Leu Gln Asp Asn Glu Leu
 145 150 155 160
 Arg Ala Leu Pro Pro Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu
 165 170 175
 Ser His Asn Ser Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala
 180 185 190

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Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp
 195 200 205
 Glu Gly Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser
 210 215 220
 Asp Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly
 225 230 235 240
 Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu Arg
 245 250 255
 Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp Val Ser
 260 265 270
 Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly Leu Phe Pro
 275 280 285
 Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe Asn Cys Val Cys
 290 295 300
 Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu Ser His Val Thr Leu
 305 310 315 320
 Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro Pro Lys Asn Ala Gly
 325 330 335
 Arg Leu Leu Leu Glu Leu Asp Tyr Ala Asp Phe Gly Cys Pro Ala Thr
 340 345 350
 Thr Thr Thr Ala Thr Val Pro Thr Thr Arg Pro Val Val Arg Glu Pro
 355 360 365
 Thr Ala Leu Ser Ser Ser Leu Ala Pro Thr Trp Leu Ser Pro Thr Ala
 370 375 380
 Pro Ala Thr Glu Ala Pro Ser Pro Pro Ser Thr Ala Pro Pro Thr Val
 385 390 395 400
 Gly Pro Val Pro Gln Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn
 405 410 415
 Gly Gly Thr Cys His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys
 420 425 430
 Pro Glu Gly Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly
 435 440 445
 Thr Arg Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu
 450 455 460
 Thr Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu
 465 470 475 480
 Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg Leu
 485 490 495
 Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr Leu Arg
 500 505 510

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Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro Asn
 515 520 525

Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro Gly Arg Val Pro
 530 535 540

Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr Pro Pro Ala Val His
 545 550 555 560

Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu Gly Asn Leu Pro Leu
 565 570 575

Leu Ile Ala Pro Ala Leu Ala Ala Val Leu Leu Ala Ala Leu Ala Ala
 580 585 590

Val Gly Ala Ala Tyr Cys Val Arg Arg Gly Arg Ala Met Ala Ala Ala
 595 600 605

Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Ala Gly Pro Leu Glu Leu
 610 615 620

Glu Gly Val Lys Val Pro Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly
 625 630 635 640

Gly Gly Glu Ala Leu Pro Ser Gly Ser Glu Cys Glu Val Pro Leu Met
 645 650 655

Gly Phe Pro Gly Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr
 660 665 670

Ile

<210> 60

<211> 2019

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2019)

<400> 60

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 Met Cys Ser Arg Val Pro Leu Leu Leu Pro Leu Leu Leu Leu Ala
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ctg ggg cct ggg gtg cag ggc tgc cca tcc ggc tgc cag tgc agc cag 96
 Leu Gly Pro Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys Ser Gln
 20 25 30

cca cag aca gtc ttc tgc act gcc cgc cag ggg acc acg gtg ccc cga 144
 Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr Val Pro Arg
 35 40 45

gac gtg cca ccc gac acg gtg ggg ctg tac gtc ttt gag aac ggc atc 192
 Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Val Phe Glu Asn Gly Ile
 50 55 60

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acc atg ctc gac gca ggc agc ttt gcc ggc ctg ccg ggc ctg cag ctc	240
Thr Met Leu Asp Ala Gly Ser Phe Ala Gly Leu Pro Gly Leu Gln Leu	
65 70 75 80	
ctg gac ctg tca cag aac cag atc gcc agc ctg ccc agc ggg gtc ttc	288
Leu Asp Leu Ser Gln Asn Gln Ile Ala Ser Leu Pro Ser Gly Val Phe	
85 90 95	
cag cca ctc gcc aac ctc agc aac ctg gac ctg acg gcc aac agg ctg	336
Gln Pro Leu Ala Asn Leu Ser Asn Leu Asp Leu Thr Ala Asn Arg Leu	
100 105 110	
cat gaa atc acc aat gag acc ttc cgt ggc ctg cgg cgc ctc gag cgc	384
His Glu Ile Thr Asn Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu Arg	
115 120 125	
ctc tac ctg ggc aag aac cgc atc cgc cac atc cag cct ggt gcc ttc	432
Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile Gln Pro Gly Ala Phe	
130 135 140	
gac acg ctc gac cgc ctc ctg gag ctc aag ctg cag gac aac gag ctg	480
Asp Thr Leu Asp Arg Leu Leu Glu Leu Lys Leu Gln Asp Asn Glu Leu	
145 150 155 160	
cgg gca ctg ccc ccg ctg cgc ctg ccc cgc ctg ctg ctg ctg gac ctc	528
Arg Ala Leu Pro Pro Leu Arg Leu Pro Arg Leu Leu Leu Leu Asp Leu	
165 170 175	
agc cac aac agc ctc ctg gcc ctg gag ccc ggc atc ctg gac act gcc	576
Ser His Asn Ser Leu Leu Ala Leu Glu Pro Gly Ile Leu Asp Thr Ala	
180 185 190	
aac gtg gag gcg ctg cgg ctg gct ggt ctg ggg ctg cag cag ctg gac	624
Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly Leu Gln Gln Leu Asp	
195 200 205	
gag ggg ctc ttc agc cgc ttg cgc aac ctc cac gac ctg gat gtg tcc	672
Glu Gly Leu Phe Ser Arg Leu Arg Asn Leu His Asp Leu Asp Val Ser	
210 215 220	
gac aac cag ctg gag cga gtg cca cct gtg atc cga ggc ctc cgg ggc	720
Asp Asn Gln Leu Glu Arg Val Pro Pro Val Ile Arg Gly Leu Arg Gly	
225 230 235 240	
ctg acg cgc ctg cgg ctg gcc ggc aac acc cgc att gcc cag ctg cgg	768
Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg Ile Ala Gln Leu Arg	
245 250 255	
ccc gag gac ctg gcc ggc ctg gct gcc ctg cag gag ctg gat gtg agc	816
Pro Glu Asp Leu Ala Gly Leu Ala Ala Leu Gln Glu Leu Asp Val Ser	
260 265 270	
aac cta agc ctg cag gcc ctg cct ggc gac ctc tcg ggc ctc ttc ccc	864
Asn Leu Ser Leu Gln Ala Leu Pro Gly Asp Leu Ser Gly Leu Phe Pro	
275 280 285	
cgc ctg cgg ctg ctg gca gct gcc cgc aac ccc ttc aac tgc gtg tgc	912
Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro Phe Asn Cys Val Cys	
290 295 300	

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ccc ctg agc tgg ttt ggc ccc tgg gtg cgc gag agc cac gtc aca ctg	960
Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu Ser His Val Thr Leu	
305 310 315 320	
gcc agc cct gag gag acg cgc tgc cac ttc ccg ccc aag aac gct ggc	1008
Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro Pro Lys Asn Ala Gly	
325 330 335	
cgg ctg ctc ctg gag ctt gac tac gcc gac ttt ggc tgc cca gcc acc	1056
Arg Leu Leu Leu Glu Leu Asp Tyr Ala Asp Phe Gly Cys Pro Ala Thr	
340 345 350	
acc acc aca gcc aca gtg ccc acc acg agg ccc gtg gtg cgg gag ccc	1104
Thr Thr Thr Ala Thr Val Pro Thr Thr Arg Pro Val Val Arg Glu Pro	
355 360 365	
aca gcc ttg tct tct agc ttg gct cct acc tgg ctt agc ccc aca gcg	1152
Thr Ala Leu Ser Ser Ser Leu Ala Pro Thr Trp Leu Ser Pro Thr Ala	
370 375 380	
ccg gcc act gag gcc ccc agc ccg ccc tcc act gcc cca ccg act gta	1200
Pro Ala Thr Glu Ala Pro Ser Pro Pro Ser Thr Ala Pro Pro Thr Val	
385 390 395 400	
ggg cct gtc ccc cag ccc cag gac tgc cca ccg tcc acc tgc ctc aat	1248
Gly Pro Val Pro Gln Pro Gln Asp Cys Pro Pro Ser Thr Cys Leu Asn	
405 410 415	
ggg ggc aca tgc cac ctg ggg aca cgg cac cac ctg gcg tgc ttg tgc	1296
Gly Gly Thr Cys His Leu Gly Thr Arg His His Leu Ala Cys Leu Cys	
420 425 430	
ccc gaa ggc ttc acg ggc ctg tac tgt gag agc cag atg ggg cag ggg	1344
Pro Glu Gly Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly	
435 440 445	
aca cgg ccc agc cct aca cca gtc acg ccg agg cca cca cgg tcc ctg	1392
Thr Arg Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu	
450 455 460	
acc ctg ggc atc gag ccg gtg agc ccc acc tcc ctg cgc gtg ggg ctg	1440
Thr Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu	
465 470 475 480	
cag cgc tac ctc cag ggg agc tcc gtg cag ctc agg agc ctc cgt ctc	1488
Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg Leu	
485 490 495	
acc tat cgc aac cta tcg ggc cct gat aag cgg ctg gtg acg ctg cga	1536
Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr Leu Arg	
500 505 510	
ctg cct gcc tcg ctc gct gag tac acg gtc acc cag ctg cgg ccc aac	1584
Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu Arg Pro Asn	
515 520 525	
gcc act tac tcc gtc tgt gtc atg cct ttg ggg ccc ggg cgg gtg ccg	1632
Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro Gly Arg Val Pro	
530 535 540	

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gag ggc gag gag gcc tgc ggg gag gcc cat aca ccc cca gcc gtc cac	1680
Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr Pro Pro Ala Val His	
545 550 555 560	
tcc aac cac gcc cca gtc acc cag gcc cgc gag ggc aac ctg ccg ctc	1728
Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu Gly Asn Leu Pro Leu	
565 570 575	
ctc att gcg ccc gcc ctg gcc gcg gtg ctc ctg gcc gcg ctg gct gcg	1776
Leu Ile Ala Pro Ala Leu Ala Ala Val Leu Leu Ala Ala Leu Ala Ala	
580 585 590	
gtg ggg gca gcc tac tgt gtg cgg cgg ggg cgg gcc atg gca gca gcg	1824
Val Gly Ala Ala Tyr Cys Val Arg Arg Gly Arg Ala Met Ala Ala Ala	
595 600 605	
gct cag gac aaa ggg cag gtg ggg cca ggg gct ggg ccc ctg gaa ctg	1872
Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Ala Gly Pro Leu Glu Leu	
610 615 620	
gag gga gtg aag gtc ccc ttg gag cca ggc ccg aag gca aca gag ggc	1920
Glu Gly Val Lys Val Pro Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly	
625 630 635 640	
ggc ttc cca ggg cct ggc ctc cag tca ccc ctc cac gca aag ccc tac	2016
Gly Phe Pro Gly Pro Gly Leu Gln Ser Pro Leu His Ala Lys Pro Tyr	
660 665 670	
atc	2019
Ile	
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<212> PRT	
<213> Homo sapiens	
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Gln Pro Phe Pro Cys Pro Pro Ala Cys Lys Cys Val Phe Arg Asp Ala	
20 25 30	
Ala Gln Cys Ser Gly Gly Asp Val Ala Arg Ile Ser Ala Leu Gly Leu	
35 40 45	
Pro Thr Asn Leu Thr His Ile Leu Leu Phe Gly Met Gly Arg Gly Val	
50 55 60	
Leu Gln Ser Gln Ser Phe Ser Gly Met Thr Val Leu Gln Arg Leu Met	
65 70 75 80	
Ile Ser Asp Ser His Ile Ser Ala Val Ala Pro Gly Thr Phe Ser Asp	
85 90 95	

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Leu Ile Lys Leu Lys Thr Leu Arg Leu Ser Arg Asn Lys Ile Thr His
 100 105 110
 Leu Pro Gly Ala Leu Leu Asp Lys Met Val Leu Leu Glu Gln Leu Phe
 115 120 125
 Leu Asp His Asn Ala Leu Arg Gly Ile Asp Gln Asn Met Phe Gln Lys
 130 135 140
 Leu Val Asn Leu Gln Glu Leu Ala Leu Asn Gln Asn Gln Leu Asp Phe
 145 150 155 160
 Leu Pro Ala Ser Leu Phe Thr Asn Leu Glu Asn Leu Lys Leu Leu Asp
 165 170 175
 Leu Ser Gly Asn Asn Leu Thr His Leu Pro Lys Gly Leu Leu Gly Ala
 180 185 190
 Gln Ala Lys Leu Glu Arg Leu Leu Leu His Ser Asn Arg Leu Val Ser
 195 200 205
 Leu Asp Ser Gly Leu Leu Asn Ser Leu Gly Ala Leu Thr Glu Leu Gln
 210 215 220
 Phe His Arg Asn His Ile Arg Ser Ile Ala Pro Gly Ala Phe Asp Arg
 225 230 235 240
 Leu Pro Asn Leu Ser Ser Leu Thr Leu Ser Arg Asn His Leu Ala Phe
 245 250 255
 Leu Pro Ser Ala Leu Phe Leu His Ser His Asn Leu Thr Leu Leu Thr
 260 265 270
 Leu Phe Glu Asn Pro Leu Ala Glu Leu Pro Gly Val Leu Phe Gly Glu
 275 280 285
 Met Gly Gly Leu Gln Glu Leu Trp Leu Asn Arg Thr Gln Leu Arg Thr
 290 295 300
 Leu Pro Ala Ala Ala Phe Arg Asn Leu Ser Arg Leu Arg Tyr Leu Gly
 305 310 315 320
 Val Thr Leu Ser Pro Arg Leu Ser Ala Leu Pro Gln Gly Ala Phe Gln
 325 330 335
 Gly Leu Gly Glu Leu Gln Val Leu Ala Leu His Ser Asn Gly Leu Thr
 340 345 350
 Ala Leu Pro Asp Gly Leu Leu Arg Gly Leu Gly Lys Leu Arg Gln Val
 355 360 365
 Ser Leu Arg Arg Asn Arg Leu Arg Ala Leu Pro Arg Ala Leu Phe Arg
 370 375 380
 Asn Leu Ser Ser Leu Glu Ser Val Gln Leu Asp His Asn Gln Leu Glu
 385 390 395 400
 Thr Leu Pro Gly Asp Val Phe Gly Ala Leu Pro Arg Leu Thr Glu Val
 405 410 415

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Leu Leu Gly His Asn Ser Trp Arg Cys Asp Cys Gly Leu Gly Pro Phe
420 425 430

Leu Gly Trp Leu Arg Gln His Leu Gly Leu Val Gly Gly Glu Glu Pro
435 440 445

Pro Arg Cys Ala Gly Pro Gly Ala His Ala Gly Leu Pro Leu Trp Ala
450 455 460

Leu Pro Gly Gly Asp Ala Glu Cys Pro Gly Pro Arg Gly Pro Pro Pro
465 470 475 480

Arg Pro Ala Ala Asp Ser Ser Ser Glu Ala Pro Val His Pro Ala Leu
485 490 495

Ala Pro Asn Ser Ser Glu Pro Trp Val Trp Ala Gln Pro Val Thr Thr
500 505 510

Gly Lys Gly Gln Asp His Ser Pro Phe Trp Gly Phe Tyr Phe Leu Leu
515 520 525

Leu Ala Val Gln Ala Met Ile Thr Val Ile Ile Val Phe Ala Met Ile
530 535 540

Lys Ile Gly Gln Leu Phe Arg Lys Leu Ile Arg Glu Arg Ala Leu Gly
545 550 555 560

<210> 62
<211> 605
<212> PRT
<213> Papio hamadryas

<400> 62
Met Ala Leu Arg Lys Gly Gly Leu Ala Leu Ala Leu Leu Leu Ser
1 5 10 15

Trp Val Ala Leu Gly Pro Arg Ser Leu Glu Gly Ala Glu Pro Gly Thr
20 25 30

Pro Gly Glu Ala Glu Gly Pro Ala Cys Pro Ala Thr Cys Ala Cys Ser
35 40 45

Tyr Asp Asp Glu Val Asn Glu Leu Ser Val Phe Cys Ser Ser Arg Asn
50 55 60

Leu Thr Arg Leu Pro Asp Gly Ile Pro Gly Gly Thr Gln Ala Leu Trp
65 70 75 80

Leu Asp Ser Asn Asn Leu Ser Ser Ile Pro Pro Ala Ala Phe Arg Asn
85 90 95

Leu Ser Ser Leu Ala Phe Leu Asn Leu Gln Gly Gly Gln Leu Gly Ser
100 105 110

Leu Glu Pro Gln Ala Leu Leu Gly Leu Glu Asn Leu Cys His Leu His
115 120 125

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Leu Glu Arg Asn Gln Leu Arg Ser Leu Ala Val Gly Thr Phe Ala Tyr
 130 135 140
 Thr Pro Ala Leu Ala Leu Leu Gly Leu Ser Asn Asn Arg Leu Ser Arg
 145 150 155 160
 Leu Glu Asp Gly Leu Phe Glu Gly Leu Gly Asn Leu Trp Asp Leu Asn
 165 170 175
 Leu Gly Trp Asn Ser Leu Ala Val Leu Pro Asp Ala Ala Phe Arg Gly
 180 185 190
 Leu Gly Gly Leu Arg Glu Leu Val Leu Ala Gly Asn Arg Leu Ala Tyr
 195 200 205
 Leu Gln Pro Ala Leu Phe Ser Gly Leu Ala Glu Leu Arg Glu Leu Asp
 210 215 220
 Leu Ser Arg Asn Ala Leu Arg Ala Ile Lys Ala Asn Val Phe Ala Gln
 225 230 235 240
 Leu Pro Arg Leu Gln Lys Leu Tyr Leu Asp Arg Asn Leu Ile Ala Ala
 245 250 255
 Val Ala Pro Gly Ala Phe Leu Gly Leu Lys Ala Leu Arg Trp Leu Asp
 260 265 270
 Leu Ser His Asn Arg Val Ala Gly Leu Leu Glu Asp Thr Phe Pro Gly
 275 280 285
 Leu Leu Gly Leu Arg Val Leu Arg Leu Ser His Asn Ala Ile Ala Ser
 290 295 300
 Leu Arg Pro Arg Thr Phe Glu Asp Leu His Phe Leu Glu Glu Leu Gln
 305 310 315 320
 Leu Gly His Asn Arg Ile Arg Gln Leu Ala Glu Arg Ser Phe Glu Gly
 325 330 335
 Leu Gly Gln Leu Glu Val Leu Thr Leu Asp His Asn Gln Leu Gln Glu
 340 345 350
 Val Lys Val Gly Ala Phe Leu Gly Leu Thr Asn Val Ala Val Met Asn
 355 360 365
 Leu Ser Gly Asn Cys Leu Arg Asn Leu Pro Glu Gln Val Phe Arg Gly
 370 375 380
 Leu Gly Lys Leu His Ser Leu His Leu Glu Gly Ser Cys Leu Gly Arg
 385 390 395 400
 Ile Arg Pro His Thr Phe Ala Gly Leu Ser Gly Leu Arg Arg Leu Phe
 405 410 415
 Leu Lys Asp Asn Gly Leu Val Gly Ile Glu Glu Gln Ser Leu Trp Gly
 420 425 430
 Leu Ala Glu Leu Leu Glu Leu Asp Leu Thr Ser Asn Gln Leu Thr His
 435 440 445

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<400> 63
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
  1             5             10            15
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Xaa Xaa Xaa Xaa Xaa Xaa
20

<210> 64
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaas at positions 2-7, 9-15, 17-28 and 32-45, if
present, may be any amino acid

<220>
<223> Xaa at position 30 may be any amino acid

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 64
Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
35 40 45

<210> 65
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Xaas at positions 2-5, 7-11, 13-18, 24 and 26-33
may be any amino acid

<220>
<223> Xaas at positions 19-22 and 24-37, if present, may
be any amino acid

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 65
Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Cys
35

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<210> 66
<211> 73
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Consensus
sequence

<400> 66
Pro Ser Pro Pro Arg Asn Leu Arg Val Thr Asp Ile Thr Pro Thr Ser
1 5 10 15
Ile Thr Val Ser Trp Thr Pro Pro Glu Gly Asn Gly Pro Ile Thr Gly
20 25 30
Tyr Arg Ile Gln Tyr Arg Trp Pro Val Asn Asp Asn Glu Trp Asn Glu
35 40 45
Phe Asn Val Pro Arg Thr Thr Asn Ser Tyr Thr Ile Thr Asn Leu Arg
50 55 60
Pro Gly Thr Glu Tyr Glu Phe Arg Val
65 70

<210> 67
<211> 2815
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (197)..(2215)

<400> 67
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acgggacgca gcagcctctg gatcccggga ccccggacct ctcaggaccg gccagaggtg 120
aaggactgag gcccactga ggccttggac cgcaccgcct ggctccttca gccgcagtcg 180
tctcctggga cagaag atg cac tcc agg agc tgc ctg cca cct ctc ctg ttg 232
Met His Ser Arg Ser Cys Leu Pro Pro Leu Leu Leu
1 5 10
ttg ctt ctg gtg ctc ctg ggg tct gga gta cag ggt tgc cca tca ggc 280
Leu Leu Leu Val Leu Leu Gly Ser Gly Val Gln Gly Cys Pro Ser Gly
15 20 25
tgc cag tgc aac cag cca cag aca gtc ttc tgc act gcc cgt cag gga 328
Cys Gln Cys Asn Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly
30 35 40
acc aca gtg ccc cga gac gtg cca cct gac aca gtg ggc ctg tac atc 376
Thr Thr Val Pro Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Ile
45 50 55 60

- 80 -

ttt gag aac ggc atc acg aca ctt gat gtg ggc tgt ttt gct ggc ctt	424
Phe Glu Asn Gly Ile Thr Thr Leu Asp Val Gly Cys Phe Ala Gly Leu	
65 70 75	
ccg ggc ctg cag ctt ctg gac ttg tca cag aac cag atc act agc ctg	472
Pro Gly Leu Gln Leu Leu Asp Leu Ser Gln Asn Gln Ile Thr Ser Leu	
80 85 90	
ccc ggg ggc atc ttt cag cca ctt gtt aac ctc agt aac ctg gac ctg	520
Pro Gly Gly Ile Phe Gln Pro Leu Val Asn Leu Ser Asn Leu Asp Leu	
95 100 105	
act gcc aac aaa ctg cac gag atc tcc aac gag acc ttc cgt ggc ctg	568
Thr Ala Asn Lys Leu His Glu Ile Ser Asn Glu Thr Phe Arg Gly Leu	
110 115 120	
cgg cgc ctg gag cgc ctc tac ctg ggc aag aac cga att cgc cac atc	616
Arg Arg Leu Glu Arg Leu Tyr Leu Gly Lys Asn Arg Ile Arg His Ile	
125 130 135 140	
caa ccg ggt gcc ttc gac gcg ctt gat cgc ctc ctg gag ctc aag ctg	664
Gln Pro Gly Ala Phe Asp Ala Leu Asp Arg Leu Leu Glu Leu Lys Leu	
145 150 155	
cca gac aat gag ctt cgg gtg ttg ccc cca ttg cac ttg ccc cgc ctg	712
Pro Asp Asn Glu Leu Arg Val Leu Pro Pro Leu His Leu Pro Arg Leu	
160 165 170	
ctg ctg ctt gac ctc agc cac aac agc atc cca gcc ctg gaa gcc gga	760
Leu Leu Leu Asp Leu Ser His Asn Ser Ile Pro Ala Leu Glu Ala Gly	
175 180 185	
ata ctg gat acc gcc aat gta gag gca ttg agg ttg gct ggc cta ggg	808
Ile Leu Asp Thr Ala Asn Val Glu Ala Leu Arg Leu Ala Gly Leu Gly	
190 195 200	
ctg cgg cag ctg gat gag ggg ctt ttt ggc cgc ctt ctc aac ctc cat	856
Leu Arg Gln Leu Asp Glu Gly Leu Phe Gly Arg Leu Leu Asn Leu His	
205 210 215 220	
gac ttg gat gtt tct gac aac cag ttg gag cat atg cca tct gtg att	904
Asp Leu Asp Val Ser Asp Asn Gln Leu Glu His Met Pro Ser Val Ile	
225 230 235	
caa ggc ctg cgt ggc ctg aca cgc ctg cgg ctg gct ggc aac acc cgt	952
Gln Gly Leu Arg Gly Leu Thr Arg Leu Arg Leu Ala Gly Asn Thr Arg	
240 245 250	
att gcc cag ata cgg ccc gag gac ctc gct ggt ctg act gcc cta cag	1000
Ile Ala Gln Ile Arg Pro Glu Asp Leu Ala Gly Leu Thr Ala Leu Gln	
255 260 265	
gaa ttg gat gtg agc aac cta agc ctg cag gcc ctg ccc agt gac ctc	1048
Glu Leu Asp Val Ser Asn Leu Ser Leu Gln Ala Leu Pro Ser Asp Leu	
270 275 280	
tcg agt ctc ttt ccc cgc ctg cgc ctc tta gca gct gcc agg aac ccc	1096
Ser Ser Leu Phe Pro Arg Leu Arg Leu Leu Ala Ala Ala Arg Asn Pro	
285 290 295 300	

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ttc aac tgc ttg tgc ccc ttg agc tgg ttt ggt cct tgg gtg cgt gag	1144
Phe Asn Cys Leu Cys Pro Leu Ser Trp Phe Gly Pro Trp Val Arg Glu	
305 310 315	
aac cat gtt gtg ttg gcc agc cct gag gag acg cgt tgt cac ttt cca	1192
Asn His Val Val Leu Ala Ser Pro Glu Glu Thr Arg Cys His Phe Pro	
320 325 330	
ccc aag aat gct ggc cga ctg ctc ctg gat ctg gat tat gca gat ttt	1240
Pro Lys Asn Ala Gly Arg Leu Leu Asp Leu Asp Tyr Ala Asp Phe	
335 340 345	
ggc tgc cca gtc acc act acc acg gcc aca gta cct act ata agg tct	1288
Gly Cys Pro Val Thr Thr Thr Thr Ala Thr Val Pro Thr Ile Arg Ser	
350 355 360	
act atc agg gaa ccc aca ctt tca act tct agc caa gct ccc acc tgg	1336
Thr Ile Arg Glu Pro Thr Leu Ser Thr Ser Ser Gln Ala Pro Thr Trp	
365 370 375 380	
ccc agc ctc aca gag cca act acc cag gcc tcc acc gta cta tcg act	1384
Pro Ser Leu Thr Glu Pro Thr Thr Gln Ala Ser Thr Val Leu Ser Thr	
385 390 395	
gcc cca cca acc atg agg cca gct cct cag ccc cag gac tgt cca gca	1432
Ala Pro Pro Thr Met Arg Pro Ala Pro Gln Pro Gln Asp Cys Pro Ala	
400 405 410	
tcc atc tgc ctg aat ggt ggt agc tgc cgt ttg gga gca aga cac cac	1480
Ser Ile Cys Leu Asn Gly Gly Ser Cys Arg Leu Gly Ala Arg His His	
415 420 425	
tgg gag tgc cta tgc cct gag ggc ttc att ggc ctg tac tgt gag agt	1528
Trp Glu Cys Leu Cys Pro Glu Gly Phe Ile Gly Leu Tyr Cys Glu Ser	
430 435 440	
cca gtg gag caa ggg atg aag ccc agc tcc ata cca gac act cca agg	1576
Pro Val Glu Gln Gly Met Lys Pro Ser Ser Ile Pro Asp Thr Pro Arg	
445 450 455 460	
ccc cct cca ctg ctg cct ctc agc att gag ccg gtg agc ccc acc tcc	1624
Pro Pro Pro Leu Leu Pro Leu Ser Ile Glu Pro Val Ser Pro Thr Ser	
465 470 475	
ttg cgt gtg aag ctg cag cgc tac ttg cag ggt aac act gtg cag cta	1672
Leu Arg Val Lys Leu Gln Arg Tyr Leu Gln Gly Asn Thr Val Gln Leu	
480 485 490	
cgg agc ctc cgg ctc acc tat cgc aac ctg tct ggc cct gac aaa cga	1720
Arg Ser Leu Arg Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg	
495 500 505	
ctg gtg aca tta cgg ctg cct gct tca ctt gca gag tat aca gtc acc	1768
Leu Val Thr Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr	
510 515 520	
cag ctg cga ccc aat gcc acc tat tct atc tgt gtc aca ccc ttg gga	1816
Gln Leu Arg Pro Asn Ala Thr Tyr Ser Ile Cys Val Thr Pro Leu Gly	
525 530 535 540	

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gct gga cgg aca cct gaa ggt gag gag gcc tgt ggg gag gcc aac act 1864
 Ala Gly Arg Thr Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala Asn Thr
 545 550 555

tcc cag gca gtc cgc tct aac cat gcc cca gtt acc cag gcc cgt gag 1912
 Ser Gln Ala Val Arg Ser Asn His Ala Pro Val Thr Gln Ala Arg Glu
 560 565 570

ggc aac ctg cca ctc ctc att gcg cct gcc ctg gct gct gta ctt ctg 1960
 Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Val Leu Leu
 575 580 585

gct gtg tta gcc gct gca ggg gca gcc tac tgt gtg cgg cgg gca cgg 2008
 Ala Val Leu Ala Ala Ala Gly Ala Ala Tyr Cys Val Arg Arg Ala Arg
 590 595 600

gca act tct aca gct cag gac aaa ggg cag gtg ggg cca ggg act gga 2056
 Ala Thr Ser Thr Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Thr Gly
 605 610 615 620

ccc ctg gaa cta gag ggg gtg aaa gcc cct ttg gag cca ggc tcc aag 2104
 Pro Leu Glu Leu Glu Gly Val Lys Ala Pro Leu Glu Pro Gly Ser Lys
 625 630 635

gca aca gag gga ggt ggg gag gct ttg tca ggt ggt cct gaa tgt gag 2152
 Ala Thr Glu Gly Gly Gly Glu Ala Leu Ser Gly Gly Pro Glu Cys Glu
 640 645 650

gtg cct ctt atg ggc tac cca ggg ccc agc ctt cag ggg gtc ctc cct 2200
 Val Pro Leu Met Gly Tyr Pro Gly Pro Ser Leu Gln Gly Val Leu Pro
 655 660 665

gct aag cac tac att tagactgggtg agaaagagca gccaggggggt caggctttca 2255
 Ala Lys His Tyr Ile
 670

gtcaccaccc tctgtctgcc acagaaggaa gttctcagta tacaccacag tgcacgtgca 2315
 tgatggagct gtgggaccct ctctgggctg ggtctcatct gtaagctgct acagcccaga 2375
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 gatctttttcc catttatgct gggaaagtgt ttttcaaact cagtgacaag gactttgggtt 2735
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 aaaaaaaaaa gggcggccgc 2815

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<210> 68
 <211> 673
 <212> PRT
 <213> Mus musculus

<400> 68

Met	His	Ser	Arg	Ser	Cys	Leu	Pro	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Val
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Leu	Leu	Gly	Ser	Gly	Val	Gln	Gly	Cys	Pro	Ser	Gly	Cys	Gln	Cys	Asn
			20					25					30		
Gln	Pro	Gln	Thr	Val	Phe	Cys	Thr	Ala	Arg	Gln	Gly	Thr	Thr	Val	Pro
			35				40					45			
Arg	Asp	Val	Pro	Pro	Asp	Thr	Val	Gly	Leu	Tyr	Ile	Phe	Glu	Asn	Gly
	50					55					60				
Ile	Thr	Thr	Leu	Asp	Val	Gly	Cys	Phe	Ala	Gly	Leu	Pro	Gly	Leu	Gln
65					70					75					80
Leu	Leu	Asp	Leu	Ser	Gln	Asn	Gln	Ile	Thr	Ser	Leu	Pro	Gly	Gly	Ile
				85					90					95	
Phe	Gln	Pro	Leu	Val	Asn	Leu	Ser	Asn	Leu	Asp	Leu	Thr	Ala	Asn	Lys
			100					105					110		
Leu	His	Glu	Ile	Ser	Asn	Glu	Thr	Phe	Arg	Gly	Leu	Arg	Arg	Leu	Glu
		115					120					125			
Arg	Leu	Tyr	Leu	Gly	Lys	Asn	Arg	Ile	Arg	His	Ile	Gln	Pro	Gly	Ala
	130					135					140				
Phe	Asp	Ala	Leu	Asp	Arg	Leu	Leu	Glu	Leu	Lys	Leu	Pro	Asp	Asn	Glu
145					150					155					160
Leu	Arg	Val	Leu	Pro	Pro	Leu	His	Leu	Pro	Arg	Leu	Leu	Leu	Leu	Asp
				165					170						175
Leu	Ser	His	Asn	Ser	Ile	Pro	Ala	Leu	Glu	Ala	Gly	Ile	Leu	Asp	Thr
			180					185					190		
Ala	Asn	Val	Glu	Ala	Leu	Arg	Leu	Ala	Gly	Leu	Gly	Leu	Arg	Gln	Leu
		195					200					205			
Asp	Glu	Gly	Leu	Phe	Gly	Arg	Leu	Leu	Asn	Leu	His	Asp	Leu	Asp	Val
	210					215					220				
Ser	Asp	Asn	Gln	Leu	Glu	His	Met	Pro	Ser	Val	Ile	Gln	Gly	Leu	Arg
225					230					235					240
Gly	Leu	Thr	Arg	Leu	Arg	Leu	Ala	Gly	Asn	Thr	Arg	Ile	Ala	Gln	Ile
			245						250					255	
Arg	Pro	Glu	Asp	Leu	Ala	Gly	Leu	Thr	Ala	Leu	Gln	Glu	Leu	Asp	Val
			260					265						270	
Ser	Asn	Leu	Ser	Leu	Gln	Ala	Leu	Pro	Ser	Asp	Leu	Ser	Ser	Leu	Phe
		275					280					285			

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Pro	Arg	Leu	Arg	Leu	Leu	Ala	Ala	Ala	Arg	Asn	Pro	Phe	Asn	Cys	Leu
290						295					300				
Cys	Pro	Leu	Ser	Trp	Phe	Gly	Pro	Trp	Val	Arg	Glu	Asn	His	Val	Val
305					310					315					320
Leu	Ala	Ser	Pro	Glu	Glu	Thr	Arg	Cys	His	Phe	Pro	Pro	Lys	Asn	Ala
				325					330					335	
Gly	Arg	Leu	Leu	Leu	Asp	Leu	Asp	Tyr	Ala	Asp	Phe	Gly	Cys	Pro	Val
			340					345					350		
Thr	Thr	Thr	Thr	Ala	Thr	Val	Pro	Thr	Ile	Arg	Ser	Thr	Ile	Arg	Glu
		355					360					365			
Pro	Thr	Leu	Ser	Thr	Ser	Ser	Gln	Ala	Pro	Thr	Trp	Pro	Ser	Leu	Thr
	370					375					380				
Glu	Pro	Thr	Thr	Gln	Ala	Ser	Thr	Val	Leu	Ser	Thr	Ala	Pro	Pro	Thr
385					390					395					400
Met	Arg	Pro	Ala	Pro	Gln	Pro	Gln	Asp	Cys	Pro	Ala	Ser	Ile	Cys	Leu
				405					410					415	
Asn	Gly	Gly	Ser	Cys	Arg	Leu	Gly	Ala	Arg	His	His	Trp	Glu	Cys	Leu
			420					425					430		
Cys	Pro	Glu	Gly	Phe	Ile	Gly	Leu	Tyr	Cys	Glu	Ser	Pro	Val	Glu	Gln
		435					440					445			
Gly	Met	Lys	Pro	Ser	Ser	Ile	Pro	Asp	Thr	Pro	Arg	Pro	Pro	Pro	Leu
	450					455					460				
Leu	Pro	Leu	Ser	Ile	Glu	Pro	Val	Ser	Pro	Thr	Ser	Leu	Arg	Val	Lys
465					470					475					480
Leu	Gln	Arg	Tyr	Leu	Gln	Gly	Asn	Thr	Val	Gln	Leu	Arg	Ser	Leu	Arg
				485					490					495	
Leu	Thr	Tyr	Arg	Asn	Leu	Ser	Gly	Pro	Asp	Lys	Arg	Leu	Val	Thr	Leu
			500					505					510		
Arg	Leu	Pro	Ala	Ser	Leu	Ala	Glu	Tyr	Thr	Val	Thr	Gln	Leu	Arg	Pro
		515					520					525			
Asn	Ala	Thr	Tyr	Ser	Ile	Cys	Val	Thr	Pro	Leu	Gly	Ala	Gly	Arg	Thr
	530					535					540				
Pro	Glu	Gly	Glu	Glu	Ala	Cys	Gly	Glu	Ala	Asn	Thr	Ser	Gln	Ala	Val
545					550					555					560
Arg	Ser	Asn	His	Ala	Pro	Val	Thr	Gln	Ala	Arg	Glu	Gly	Asn	Leu	Pro
				565					570					575	
Leu	Leu	Ile	Ala	Pro	Ala	Leu	Ala	Ala	Val	Leu	Leu	Ala	Val	Leu	Ala
			580					585					590		
Ala	Ala	Gly	Ala	Ala	Tyr	Cys	Val	Arg	Arg	Ala	Arg	Ala	Thr	Ser	Thr
		595					600					605			

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Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Thr Gly Pro Leu Glu Leu
610 615 620

Glu Gly Val Lys Ala Pro Leu Glu Pro Gly Ser Lys Ala Thr Glu Gly
625 630 635 640

Gly Gly Glu Ala Leu Ser Gly Gly Pro Glu Cys Glu Val Pro Leu Met
645 650 655

Gly Tyr Pro Gly Pro Ser Leu Gln Gly Val Leu Pro Ala Lys His Tyr
660 665 670

Ile

<210> 69
<211> 2022
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(2019)

<400> 69

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ctc ctg ggg tct gga gta cag ggt tgc cca tca ggc tgc cag tgc aac	96
Leu Leu Gly Ser Gly Val Gln Gly Cys Pro Ser Gly Cys Gln Cys Asn	
20 25 30	
cag cca cag aca gtc ttc tgc act gcc cgt cag gga acc aca gtg ccc	144
Gln Pro Gln Thr Val Phe Cys Thr Ala Arg Gln Gly Thr Thr Val Pro	
35 40 45	
cga gac gtg cca cct gac aca gtg ggc ctg tac atc ttt gag aac ggc	192
Arg Asp Val Pro Pro Asp Thr Val Gly Leu Tyr Ile Phe Glu Asn Gly	
50 55 60	
atc acg aca ctt gat gtg ggc tgt ttt gct ggc ctt ccg ggc ctg cag	240
Ile Thr Thr Leu Asp Val Gly Cys Phe Ala Gly Leu Pro Gly Leu Gln	
65 70 75 80	
ctt ctg gac ttg tca cag aac cag atc act agc ctg ccc ggg ggc atc	288
Leu Leu Asp Leu Ser Gln Asn Gln Ile Thr Ser Leu Pro Gly Gly Ile	
85 90 95	
ttt cag cca ctt gtt aac ctc agt aac ctg gac ctg act gcc aac aaa	336
Phe Gln Pro Leu Val Asn Leu Ser Asn Leu Asp Leu Thr Ala Asn Lys	
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Leu His Glu Ile Ser Asn Glu Thr Phe Arg Gly Leu Arg Arg Leu Glu	
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Cys	Pro	Leu	Ser	Trp	Phe	Gly	Pro	Trp	Val	Arg	Glu	Asn	His	Val	Val	
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Gly	Arg	Leu	Leu	Leu	Asp	Leu	Asp	Tyr	Ala	Asp	Phe	Gly	Cys	Pro	Val	
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Leu	Pro	Leu	Ser	Ile	Glu	Pro	Val	Ser	Pro	Thr	Ser	Leu	Arg	Val	Lys	
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Pro	Glu	Gly	Glu	Glu	Ala	Cys	Gly	Glu	Ala	Asn	Thr	Ser	Gln	Ala	Val	
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Leu	Leu	Ile	Ala	Pro	Ala	Leu	Ala	Ala	Val	Leu	Leu	Ala	Val	Leu	Ala	
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gct	gca	ggg	gca	gcc	tac	tgt	gtg	cgg	cgg	gca	cgg	gca	act	tct	aca	1824
Ala	Ala	Gly	Ala	Ala	Tyr	Cys	Val	Arg	Arg	Ala	Arg	Ala	Thr	Ser	Thr	
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Ala Gln Asp Lys Gly Gln Val Gly Pro Gly Thr Gly Pro Leu Glu Leu
610 615 620

gag ggg gtg aaa gcc cct ttg gag cca ggc tcc aag gca aca gag gga 1920
Glu Gly Val Lys Ala Pro Leu Glu Pro Gly Ser Lys Ala Thr Glu Gly
625 630 635 640

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Gly Gly Glu Ala Leu Ser Gly Gly Pro Glu Cys Glu Val Pro Leu Met
645 650 655

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Met Ser Asp Glu
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Arg Arg Leu Pro Gly Ser Ala Val Gly Trp Leu Val Cys Gly Gly Leu
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Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val Gly Ala Lys Gln
25 30 35

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Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr Leu Ala Ala Thr
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His	Met	Leu	Asn	Val	Ala	Val	Pro	Ile	Ala	Thr	Tyr	Ser	Val	Val	Gln	
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Leu	Arg	Arg	Gln	Arg	Pro	Asp	Phe	Glu	Trp	Asn	Glu	Gly	Leu	Cys	Lys	
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Val	Phe	Val	Ser	Thr	Phe	Tyr	Thr	Leu	Thr	Leu	Ala	Thr	Cys	Phe	Ser	
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gtc	acc	tcc	ctc	tcc	tac	cac	cgc	atg	tgg	atg	gtc	tgc	tgg	cct	gtc	751
Val	Thr	Ser	Leu	Ser	Tyr	His	Arg	Met	Trp	Met	Val	Cys	Trp	Pro	Val	
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aac	tac	cgg	ctg	agc	aat	gcc	aag	aag	cag	gcg	gtg	cac	aca	gtc	atg	799
Asn	Tyr	Arg	Leu	Ser	Asn	Ala	Lys	Lys	Gln	Ala	Val	His	Thr	Val	Met	
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Gly	Ile	Trp	Met	Val	Ser	Phe	Ile	Leu	Ser	Ala	Leu	Pro	Ala	Val	Gly	
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tgg	cac	gac	acc	agc	gag	cgc	ttc	tac	acc	cat	ggc	tgc	cgc	ttc	atc	895
Trp	His	Asp	Thr	Ser	Glu	Arg	Phe	Tyr	Thr	His	Gly	Cys	Arg	Phe	Ile	
	150					155					160					
gtg	gct	gag	atc	ggc	ctg	ggc	ttt	ggc	gtc	tgc	ttc	ctg	ctg	ctg	gtg	943
Val	Ala	Glu	Ile	Gly	Leu	Gly	Phe	Gly	Val	Cys	Phe	Leu	Leu	Leu	Val	
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Gly	Gly	Ser	Val	Ala	Met	Gly	Val	Ile	Cys	Thr	Ala	Ile	Ala	Leu	Phe	
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Gln	Thr	Leu	Ala	Val	Gln	Val	Gly	Arg	Gln	Ala	Asp	His	Arg	Ala	Phe	
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Thr	Val	Pro	Thr	Ile	Val	Val	Glu	Asp	Ala	Gln	Gly	Lys	Arg	Arg	Ser	
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Ser	Ile	Asp	Gly	Ser	Glu	Pro	Ala	Lys	Thr	Ser	Leu	Gln	Thr	Thr	Gly	
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Val	Leu	Asp	Ser	Thr	Pro	Ile	Pro	Glu	Arg	Ser	Ala	Val	Arg	Gln	Gly	
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Thr	Cys	Phe	Ser	Val	Thr	Ser	Leu	Ser	Tyr	His	Arg	Met	Trp	Met	Val	100	105	110	
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Cys	Arg	Phe	Ile	Val	Ala	Glu	Ile	Gly	Leu	Gly	Phe	Gly	Val	Cys	Phe	165	170	175	
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Ile	Ala	Leu	Phe	Gln	Thr	Leu	Ala	Val	Gln	Val	Gly	Arg	Gln	Ala	Asp	195	200	205	
His	Arg	Ala	Phe	Thr	Val	Pro	Thr	Ile	Val	Val	Glu	Asp	Ala	Gln	Gly	210	215	220	
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Val	Arg	Gln	Gly	Glu	Asp	Trp	Gly	Lys	Asp	Gln	Pro	Glu	Gly	Phe	His	275	280	285	

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Cys Gly Gly Leu Ser Leu Leu Ala Asn Ala Trp Gly Ile Leu Ser Val	
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Gly Ala Lys Gln Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr	
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Leu Ala Ala Thr His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr	
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Ser Val Val Gln Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu	
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Gly Leu Cys Lys Val Phe Val Ser Thr Phe Tyr Thr Leu Thr Leu Ala	
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acc tgt ttc tct gtc acc tcc ctc tcc tac cac cgc atg tgg atg gtc	336
Thr Cys Phe Ser Val Thr Ser Leu Ser Tyr His Arg Met Trp Met Val	
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Cys Trp Pro Val Asn Tyr Arg Leu Ser Asn Ala Lys Lys Gln Ala Val	
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His Thr Val Met Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala Leu	
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Pro Ala Val Gly Trp His Asp Thr Ser Glu Arg Phe Tyr Thr His Gly	
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Leu Leu Leu Val Gly Gly Ser Val Ala Met Gly Val Ile Cys Thr Ala
180 185 190

atc gcc ctc ttc cag acg ctg gcc gtg cag gtg ggg cgc cag gcc gac 624
Ile Ala Leu Phe Gln Thr Leu Ala Val Gln Val Gly Arg Gln Ala Asp
195 200 205

cac cgc gcc ttc acc gtg ccc acc atc gtg gtg gag gac gcg cag gcc 672
His Arg Ala Phe Thr Val Pro Thr Ile Val Val Glu Asp Ala Gln Gly
210 215 220

aag cgg cgc tcc tcc atc gat ggc tcg gag ccc gcc aaa acc tct ctg 720
Lys Arg Arg Ser Ser Ile Asp Gly Ser Glu Pro Ala Lys Thr Ser Leu
225 230 235 240

cag acc acg ggc ctc gtg acc acc ata gtc ttc atc tac gac tgc ctc 768
Gln Thr Thr Gly Leu Val Thr Thr Ile Val Phe Ile Tyr Asp Cys Leu
245 250 255

atg ggc ttc cct gtg ctg gac tct acg ccc atc ccc gaa agg tct gca 816
Met Gly Phe Pro Val Leu Asp Ser Thr Pro Ile Pro Glu Arg Ser Ala
260 265 270

gtg aga cag gga gag gac tgg ggc aaa gac cag cct gag ggg ttt cat 864
Val Arg Gln Gly Glu Asp Trp Gly Lys Asp Gln Pro Glu Gly Phe His
275 280 285

cca agc agc agg caa gac tgc ctt ccc 891
Pro Ser Ser Arg Gln Asp Cys Leu Pro
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gaggcgggag cagcgagccg gagccccggg cgctcgaatg caggatgctc gtggtcccca 240
gcaccccttga gccaccagga gtgagggctg ctgctccctg agacctggct ccaaggagga 300
tgccacagcc gcctgccagc tccggtctgc acc atg agt gat gag cgg cgg ctg 354
Met Ser Asp Glu Arg Arg Leu
1 5

cct ggc agt gca gtg ggc tgg ctg gta tgt ggg ggc ctc tcc ctg ctg 402
Pro Gly Ser Ala Val Gly Trp Leu Val Cys Gly Gly Leu Ser Leu Leu
10 15 20

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gcc aat gcc tgg ggc atc ctc agc gtt ggc gcc aag cag aag aag tgg	450
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25 30 35	
aag ccc ttg gag ttc ctg ctg tgt acg ctc gcg gcc acc cac atg cta	498
Lys Pro Leu Glu Phe Leu Leu Cys Thr Leu Ala Ala Thr His Met Leu	
40 45 50 55	
aat gtg gcc gtg ccc atc gcc acc tac tcc gtg gtg cag ctg cgg cgg	546
Asn Val Ala Val Pro Ile Ala Thr Tyr Ser Val Val Gln Leu Arg Arg	
60 65 70	
cag cgc ccc gac ttc gag tgg aat gag ggt ctc tgc aag gtc ttc gtg	594
Gln Arg Pro Asp Phe Glu Trp Asn Glu Gly Leu Cys Lys Val Phe Val	
75 80 85	
tcc acc ttc tac acc ctc acc ctg gcc acc tgt ttc tct gtc acc tcc	642
Ser Thr Phe Tyr Thr Leu Thr Leu Ala Thr Cys Phe Ser Val Thr Ser	
90 95 100	
ctc tcc tac cac cgc atg tgg atg gtc tgc tgg cct gtc aac tac cgg	690
Leu Ser Tyr His Arg Met Trp Met Val Cys Trp Pro Val Asn Tyr Arg	
105 110 115	
ctg agc aat gcc aag aag cag gcg gtg cac aca gtc atg ggt atc tgg	738
Leu Ser Asn Ala Lys Lys Gln Ala Val His Thr Val Met Gly Ile Trp	
120 125 130 135	
atg gtg tcc ttc atc ctg tcg gcc ctg cct gcc gtt ggc tgg cac gac	786
Met Val Ser Phe Ile Leu Ser Ala Leu Pro Ala Val Gly Trp His Asp	
140 145 150	
acc agc gag cgc ttc tac acc cat gcc tgc cgc ttc atc gtg gct gag	834
Thr Ser Glu Arg Phe Tyr Thr His Gly Cys Arg Phe Ile Val Ala Glu	
155 160 165	
atc gcc ctg gcc ttt gcc gtc tgc ttc ctg ctg ctg gtg gcc gcc agc	882
Ile Gly Leu Gly Phe Gly Val Cys Phe Leu Leu Leu Val Gly Gly Ser	
170 175 180	
gtg gcc atg gcc gtg atc tgc aca gcc atc gcc ctc ttc cag acg ctg	930
Val Ala Met Gly Val Ile Cys Thr Ala Ile Ala Leu Phe Gln Thr Leu	
185 190 195	
gcc gtg cag gtg ggg cgc cag gcc gac cac cgc gcc ttc acc gtg ccc	978
Ala Val Gln Val Gly Arg Gln Ala Asp His Arg Ala Phe Thr Val Pro	
200 205 210 215	
acc atc gtg gtg gag gac gcg cag gcc aag cgg cgc tcc tcc atc gat	1026
Thr Ile Val Val Glu Asp Ala Gln Gly Lys Arg Arg Ser Ser Ile Asp	
220 225 230	
ggc tcg gag ccc gcc aaa acc tct ctg cag acc acg gcc ctc gtg acc	1074
Gly Ser Glu Pro Ala Lys Thr Ser Leu Gln Thr Thr Gly Leu Val Thr	
235 240 245	
acc ata gtc ttc atc tac gac tgc ctc atg gcc ttc cct gtg ctg gtg	1122
Thr Ile Val Phe Ile Tyr Asp Cys Leu Met Gly Phe Pro Val Leu Val	
250 255 260	

- 95 -

gtg	agc	ttc	agc	agc	ctg	cgg	gcc	gac	gcc	tca	gcg	ccc	tgg	atg	gca	1170
Val	Ser	Phe	Ser	Ser	Leu	Arg	Ala	Asp	Ala	Ser	Ala	Pro	Trp	Met	Ala	
	265					270					275					
ctc	tgc	gtg	ctg	tgg	tgc	tcc	gtg	gcc	cag	gcc	ctg	ctg	ctg	cct	gtg	1218
Leu	Cys	Val	Leu	Trp	Cys	Ser	Val	Ala	Gln	Ala	Leu	Leu	Leu	Pro	Val	
280					285					290					295	
ttc	ctc	tgg	gcc	tgc	gac	cgc	tac	cgg	gct	gac	ctc	aaa	gct	gtc	cgg	1266
Phe	Leu	Trp	Ala	Cys	Asp	Arg	Tyr	Arg	Ala	Asp	Leu	Lys	Ala	Val	Arg	
				300					305					310		
gag	aag	tgc	atg	gcc	ctc	atg	gcc	aac	gac	gag	gag	tca	gac	gat	gag	1314
Glu	Lys	Cys	Met	Ala	Leu	Met	Ala	Asn	Asp	Glu	Glu	Ser	Asp	Asp	Glu	
			315					320					325			
acc	agc	ctg	gaa	ggc	ggc	atc	tcc	ccg	gac	ctg	gtg	ttg	gag	cgc	tcc	1362
Thr	Ser	Leu	Glu	Gly	Gly	Ile	Ser	Pro	Asp	Leu	Val	Leu	Glu	Arg	Ser	
		330					335					340				
ctg	gac	tat	ggc	tat	gga	ggc	gat	ttt	gtg	gcc	cta	gat	agg	atg	gcc	1410
Leu	Asp	Tyr	Gly	Tyr	Gly	Gly	Asp	Phe	Val	Ala	Leu	Asp	Arg	Met	Ala	
	345					350					355					
aag	tat	gag	atc	tcc	gcc	ctg	gag	ggg	ggc	ctg	ccc	cag	ctc	tac	cca	1458
Lys	Tyr	Glu	Ile	Ser	Ala	Leu	Glu	Gly	Gly	Leu	Pro	Gln	Leu	Tyr	Pro	
360					365					370					375	
ctg	cgg	ccc	ttg	cag	gag	gac	aag	atg	caa	tac	ctg	cag	gtc	ccg	ccc	1506
Leu	Arg	Pro	Leu	Gln	Glu	Asp	Lys	Met	Gln	Tyr	Leu	Gln	Val	Pro	Pro	
				380					385					390		
acg	cgg	cgc	ttc	tcc	cac	gac	gat	gcg	gac	gtg	tgg	gcc	gcc	gtc	ccg	1554
Thr	Arg	Arg	Phe	Ser	His	Asp	Asp	Ala	Asp	Val	Trp	Ala	Ala	Val	Pro	
			395					400					405			
ctg	ccc	gcc	ttc	ctg	ccg	cgc	tgg	ggc	tcc	ggc	gag	gac	ctg	gcc	gcc	1602
Leu	Pro	Ala	Phe	Leu	Pro	Arg	Trp	Gly	Ser	Gly	Glu	Asp	Leu	Ala	Ala	
		410					415					420				
ctg	gcg	cac	ctg	gtg	ctg	cct	gcc	ggg	ccc	gag	cgg	cgc	cgc	gcc	agc	1650
Leu	Ala	His	Leu	Val	Leu	Pro	Ala	Gly	Pro	Glu	Arg	Arg	Arg	Ala	Ser	
	425					430					435					
ctc	ctg	gcc	ttc	gcg	gag	gac	gca	cca	ccg	tcc	cgc	gcg	cgc	cgc	cgc	1698
Leu	Leu	Ala	Phe	Ala	Glu	Asp	Ala	Pro	Pro	Ser	Arg	Ala	Arg	Arg	Arg	
440					445					450					455	
tcg	gcc	gag	agc	ctg	ctg	tcg	ctg	cgg	acc	tcg	gcc	ctg	gat	agc	ggc	1746
Ser	Ala	Glu	Ser	Leu	Leu	Ser	Leu	Arg	Thr	Ser	Ala	Leu	Asp	Ser	Gly	
				460					465					470		
ccg	cgg	gga	gcc	cgc	gac	tcg	ccc	ccc	ggc	agc	ccg	cgc	cgc	cgc	ccc	1794
Pro	Arg	Gly	Ala	Arg	Asp	Ser	Pro	Pro	Gly	Ser	Pro	Arg	Arg	Arg	Pro	
			475					480					485			
ggg	ccc	ggc	ccc	cgc	tcc	gcc	tcg	gcc	tcg	ctg	ctg	ccc	gac	gcc	ttc	1842
Gly	Pro	Gly	Pro	Arg	Ser	Ala	Ser	Ala	Ser	Leu	Leu	Pro	Asp	Ala	Phe	
		490					495					500				

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gcc ctg acc gcc ttc gag tgc gag cca cag gcc ctg cgc cgc ccg ccc 1890
 Ala Leu Thr Ala Phe Glu Cys Glu Pro Gln Ala Leu Arg Arg Pro Pro
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ggg ccc ttc ccc gct gcg ccc gcc gcc ccc gac ggc gca gat ccc gga 1938
 Gly Pro Phe Pro Ala Ala Pro Ala Ala Pro Asp Gly Ala Asp Pro Gly
 520 525 530 535

gag gcc ccg acg ccc cca agc agc gcc cag cgg agc cca ggg cca cgc 1986
 Glu Ala Pro Thr Pro Pro Ser Ser Ala Gln Arg Ser Pro Gly Pro Arg
 540 545 550

ccc tct gcg cac tcg cac gcc ggc tct ctg cgc ccc ggc ctg agc gcg 2034
 Pro Ser Ala His Ser His Ala Gly Ser Leu Arg Pro Gly Leu Ser Ala
 555 560 565

tcg tgg ggc gag ccc ggg ggg ctg cgc gcg gcg ggc ggc ggc ggc agc 2082
 Ser Trp Gly Glu Pro Gly Gly Leu Arg Ala Ala Gly Gly Gly Gly Ser
 570 575 580

acc agc agc ttc ctg agt tcc ccc tcc gag tcc tcg ggc tac gcc acg 2130
 Thr Ser Ser Phe Leu Ser Ser Pro Ser Glu Ser Ser Gly Tyr Ala Thr
 585 590 595

ctg cac tcg gac tcg ctg ggc tcc gcg tcc taggaccgcc ggcgcctccc 2180
 Leu His Ser Asp Ser Leu Gly Ser Ala Ser
 600 605

cacggacgcc aggcaggcca ggccgctctc cggggccgca gcaccaaaga cgcccgcttc 2240

cccccgcgc gcagacatgc gccacccttc ccaggggtga gggggcgcttg gcctcagcgt 2300

ttgtcttcgc gctcctccca gctggccttg tcccaggggc gacggctgcc ccggacgact 2360

gcgctgggca ccgcatgtcc cgggcccaggt gaggtcgggc ctggggagct gaggacatc 2420

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- 97 -

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<212> PRT

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Gly Ala Lys Gln Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr
 35 40 45

Leu Ala Ala Thr His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr
 50 55 60

Ser Val Val Gln Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu
 65 70 75 80

- 98 -

Gly Leu Cys Lys Val Phe•Val Ser Thr Phe Tyr Thr Leu Thr Leu Ala
 85 90 95

Thr Cys Phe Ser Val Thr Ser Leu Ser Tyr His Arg Met Trp Met Val
 100 105 110

Cys Trp Pro Val Asn Tyr Arg Leu Ser Asn Ala Lys Lys Gln Ala Val
 115 120 125

His Thr Val Met Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala Leu
 130 135 140

Pro Ala Val Gly Trp His Asp Thr Ser Glu Arg Phe Tyr Thr His Gly
 145 150 155 160

Cys Arg Phe Ile Val Ala Glu Ile Gly Leu Gly Phe Gly Val Cys Phe
 165 170 175

Leu Leu Leu Val Gly Gly Ser Val Ala Met Gly Val Ile Cys Thr Ala
 180 185 190

Ile Ala Leu Phe Gln Thr Leu Ala Val Gln Val Gly Arg Gln Ala Asp
 195 200 205

His Arg Ala Phe Thr Val Pro Thr Ile Val Val Glu Asp Ala Gln Gly
 210 215 220

Lys Arg Arg Ser Ser Ile Asp Gly Ser Glu Pro Ala Lys Thr Ser Leu
 225 230 235 240

Gln Thr Thr Gly Leu Val Thr Thr Ile Val Phe Ile Tyr Asp Cys Leu
 245 250 255

Met Gly Phe Pro Val Leu Val Val Ser Phe Ser Ser Leu Arg Ala Asp
 260 265 270

Ala Ser Ala Pro Trp Met Ala Leu Cys Val Leu Trp Cys Ser Val Ala
 275 280 285

Gln Ala Leu Leu Leu Pro Val Phe Leu Trp Ala Cys Asp Arg Tyr Arg
 290 295 300

Ala Asp Leu Lys Ala Val Arg Glu Lys Cys Met Ala Leu Met Ala Asn
 305 310 315 320

Asp Glu Glu Ser Asp Asp Glu Thr Ser Leu Glu Gly Gly Ile Ser Pro
 325 330 335

Asp Leu Val Leu Glu Arg Ser Leu Asp Tyr Gly Tyr Gly Gly Asp Phe
 340 345 350

Val Ala Leu Asp Arg Met Ala Lys Tyr Glu Ile Ser Ala Leu Glu Gly
 355 360 365

Gly Leu Pro Gln Leu Tyr Pro Leu Arg Pro Leu Gln Glu Asp Lys Met
 370 375 380

Gln Tyr Leu Gln Val Pro Pro Thr Arg Arg Phe Ser His Asp Asp Ala
 385 390 395 400

- 100 -

ggc gcc aag cag aag aag tgg aag ccc ttg gag ttc ctg ctg tgt acg	144
Gly Ala Lys Gln Lys Lys Trp Lys Pro Leu Glu Phe Leu Leu Cys Thr	
35 40 45	
ctc gcg gcc acc cac atg cta aat gtg gcc gtg ccc atc gcc acc tac	192
Leu Ala Ala Thr His Met Leu Asn Val Ala Val Pro Ile Ala Thr Tyr	
50 55 60	
tcc gtg gtg cag ctg cgg cgg cag cgc ccc gac ttc gag tgg aat gag	240
Ser Val Val Gln Leu Arg Arg Gln Arg Pro Asp Phe Glu Trp Asn Glu	
65 70 75 80	
ggc ctc tgc aag gtc ttc gtg tcc acc ttc tac acc ctc acc ctg gcc	288
Gly Leu Cys Lys Val Phe Val Ser Thr Phe Tyr Thr Leu Thr Leu Ala	
85 90 95	
acc tgt ttc tct gtc acc tcc ctc tcc tac cac cgc atg tgg atg gtc	336
Thr Cys Phe Ser Val Thr Ser Leu Ser Tyr His Arg Met Trp Met Val	
100 105 110	
tgc tgg cct gtc aac tac cgg ctg agc aat gcc aag aag cag gcg gtg	384
Cys Trp Pro Val Asn Tyr Arg Leu Ser Asn Ala Lys Lys Gln Ala Val	
115 120 125	
cac aca gtc atg ggt atc tgg atg gtg tcc ttc atc ctg tcg gcc ctg	432
His Thr Val Met Gly Ile Trp Met Val Ser Phe Ile Leu Ser Ala Leu	
130 135 140	
cct gcc gtt ggc tgg cac gac acc agc gag cgc ttc tac acc cat gcc	480
Pro Ala Val Gly Trp His Asp Thr Ser Glu Arg Phe Tyr Thr His Gly	
145 150 155 160	
tgc cgc ttc atc gtg gct gag atc ggc ctg ggc ttt ggc gtc tgc ttc	528
Cys Arg Phe Ile Val Ala Glu Ile Gly Leu Gly Phe Gly Val Cys Phe	
165 170 175	
ctg ctg ctg gtg ggc ggc agc gtg gcc atg ggc gtg atc tgc aca gcc	576
Leu Leu Leu Val Gly Gly Ser Val Ala Met Gly Val Ile Cys Thr Ala	
180 185 190	
atc gcc ctc ttc cag acg ctg gcc gtg cag gtg ggg cgc cag gcc gac	624
Ile Ala Leu Phe Gln Thr Leu Ala Val Gln Val Gly Arg Gln Ala Asp	
195 200 205	
cac cgc gcc ttc acc gtg ccc acc atc gtg gtg gag gac gcg cag gcc	672
His Arg Ala Phe Thr Val Pro Thr Ile Val Val Glu Asp Ala Gln Gly	
210 215 220	
aag cgg cgc tcc tcc atc gat ggc tcg gag ccc gcc aaa acc tct ctg	720
Lys Arg Arg Ser Ser Ile Asp Gly Ser Glu Pro Ala Lys Thr Ser Leu	
225 230 235 240	
cag acc acg ggc ctc gtg acc acc ata gtc ttc atc tac gac tgc ctc	768
Gln Thr Thr Gly Leu Val Thr Thr Ile Val Phe Ile Tyr Asp Cys Leu	
245 250 255	
atg ggc ttc cct gtg ctg gtg gtg agc ttc agc agc ctg cgg gcc gac	816
Met Gly Phe Pro Val Leu Val Val Ser Phe Ser Ser Leu Arg Ala Asp	
260 265 270	

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gcc tca gcg ccc tgg atg gca ctc tgc gtg ctg tgg tgc tcc gtg gcc Ala Ser Ala Pro Trp Met Ala Leu Cys Val Leu Trp Cys Ser Val Ala 275 280 285	864
cag gcc ctg ctg ctg cct gtg ttc ctc tgg gcc tgc gac cgc tac cgg Gln Ala Leu Leu Leu Pro Val Phe Leu Trp Ala Cys Asp Arg Tyr Arg 290 295 300	912
gct gac ctc aaa gct gtc cgg gag aag tgc atg gcc ctc atg gcc aac Ala Asp Leu Lys Ala Val Arg Glu Lys Cys Met Ala Leu Met Ala Asn 305 310 315 320	960
gac gag gag tca gac gat gag acc agc ctg gaa ggt ggc atc tcc ccg Asp Glu Glu Ser Asp Asp Glu Thr Ser Leu Glu Gly Gly Ile Ser Pro 325 330 335	1008
gac ctg gtg ttg gag cgc tcc ctg gac tat ggc tat gga ggt gat ttt Asp Leu Val Leu Glu Arg Ser Leu Asp Tyr Gly Tyr Gly Gly Asp Phe 340 345 350	1056
gtg gcc cta gat agg atg gcc aag tat gag atc tcc gcc ctg gag ggg Val Ala Leu Asp Arg Met Ala Lys Tyr Glu Ile Ser Ala Leu Glu Gly 355 360 365	1104
ggc ctg ccc cag ctc tac cca ctg cgg ccc ttg cag gag gac aag atg Gly Leu Pro Gln Leu Tyr Pro Leu Arg Pro Leu Gln Glu Asp Lys Met 370 375 380	1152
caa tac ctg cag gtc ccg ccc acg cgg cgc ttc tcc cac gac gat gcg Gln Tyr Leu Gln Val Pro Pro Thr Arg Arg Phe Ser His Asp Asp Ala 385 390 395 400	1200
gac gtg tgg gcc gcc gtc ccg ctg ccc gcc ttc ctg ccg cgc tgg ggc Asp Val Trp Ala Ala Val Pro Leu Pro Ala Phe Leu Pro Arg Trp Gly 405 410 415	1248
tcc ggc gag gac ctg gcc gcc ctg gcg cac ctg gtg ctg cct gcc ggg Ser Gly Glu Asp Leu Ala Ala Leu Ala His Leu Val Leu Pro Ala Gly 420 425 430	1296
ccc gag cgg cgc cgc gcc agc ctc ctg gcc ttc gcg gag gac gca cca Pro Glu Arg Arg Arg Ala Ser Leu Leu Ala Phe Ala Glu Asp Ala Pro 435 440 445	1344
ccg tcc cgc gcg cgc cgc cgc tcg gcc gag agc ctg ctg tcg ctg cgg Pro Ser Arg Ala Arg Arg Arg Ser Ala Glu Ser Leu Leu Ser Leu Arg 450 455 460	1392
acc tcg gcc ctg gat agc ggc ccg cgg gga gcc cgc gac tcg ccc ccc Thr Ser Ala Leu Asp Ser Gly Pro Arg Gly Ala Arg Asp Ser Pro Pro 465 470 475 480	1440
ggc agc ccg cgc cgc cgc ccc ggg ccc ggc ccc cgc tcc gcc tcg gcc Gly Ser Pro Arg Arg Arg Pro Gly Pro Gly Pro Arg Ser Ala Ser Ala 485 490 495	1488
tcg ctg ctg ccc gac gcc ttc gcc ctg acc gcc ttc gag tgc gag cca Ser Leu Leu Pro Asp Ala Phe Ala Leu Thr Ala Phe Glu Cys Glu Pro 500 505 510	1536

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cag gcc ctg cgc cgc ccg ccc ggg ccc ttc ccc gct gcg ccc gcc gcc 1584
 Gln Ala Leu Arg Arg Pro Pro Gly Pro Phe Pro Ala Ala Pro Ala Ala
 515 520 525

ccc gac ggc gca gat ccc gga gag gcc ccg acg ccc cca agc agc gcc 1632
 Pro Asp Gly Ala Asp Pro Gly Glu Ala Pro Thr Pro Pro Ser Ser Ala
 530 535 540

cag cgg agc cca ggg cca cgc ccc tct gcg cac tcg cac gcc ggc tct 1680
 Gln Arg Ser Pro Gly Pro Arg Pro Ser Ala His Ser His Ala Gly Ser
 545 550 555 560

ctg cgc ccc ggc ctg agc gcg tcg tgg ggc gag ccc ggg ggg ctg cgc 1728
 Leu Arg Pro Gly Leu Ser Ala Ser Trp Gly Glu Pro Gly Gly Leu Arg
 565 570 575

gcg gcg ggc ggc ggc ggc agc acc agc agc ttc ctg agt tcc ccc tcc 1776
 Ala Ala Gly Gly Gly Gly Ser Thr Ser Ser Phe Leu Ser Ser Pro Ser
 580 585 590

gag tcc tcg ggc tac gcc acg ctg cac tcg gac tcg ctg ggc tcc gcg 1824
 Glu Ser Ser Gly Tyr Ala Thr Leu His Ser Asp Ser Leu Gly Ser Ala
 595 600 605

tcc 1827
 Ser

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<211> 177

<212> PRT

<213> Homo sapiens

<220>

<223> Xaas at positions 38, 55 and 56 may be any amino acid

<400> 76

Gly Asn Ile Leu Val Ile Trp Val Ile Cys Arg Tyr Arg Arg Met Arg
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Thr Pro Met Asn Tyr Phe Ile Val Asn Leu Ala Val Ala Asp Leu Leu
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Phe Ser Leu Phe Thr Xaa Met Pro Phe Trp Met Val Tyr Tyr Val Met
 35 40 45

Gln Gly Arg Trp Pro Phe Xaa Xaa Gly Asp Phe Met Cys Arg Ile Trp
 50 55 60

Met Tyr Phe Asp Tyr Met Asn Met Tyr Ala Ser Ile Phe Phe Leu Thr
 65 70 75 80

Cys Ile Ser Ile Asp Arg Tyr Leu Trp Ala Ile Cys His Pro Met Arg
 85 90 95

Tyr Met Arg Trp Met Thr Pro Arg His Arg Ala Trp Val Met Ile Ile
 100 105 110

- 103 -

Ile Ile Trp Val Met Ser Phe Leu Ile Ser Met Pro Pro Phe Leu Met
 115 120 125

Phe Arg Trp Ser Thr Tyr Arg Asp Glu Asn Glu Trp Asn Met Thr Trp
 130 135 140

Cys Met Ile Tyr Asp Trp Pro Glu Trp Met Trp Arg Trp Tyr Val Ile
 145 150 155 160

Leu Met Thr Ile Ile Met Gly Phe Tyr Ile Pro Met Ile Ile Met Leu
 165 170 175

Phe

<210> 77
 <211> 107
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Xaa at position 84 may be any amino acid

<400> 77
 Ile Gln Glu Arg Met Asn Glu Leu Asn Asp Arg Trp Glu Arg Leu Lys
 1 5 10 15
 Glu Leu Met Glu Gln Arg Arg Gln Met Leu Glu Asp Ser Met Arg Leu
 20 25 30
 Gln Gln Phe Phe Arg Asp Met Asp Glu Glu Glu Ser Trp Ile Asn Glu
 35 40 45
 Lys Glu Gln Ile Leu Asn Ser Asp Asp Tyr Gly Lys Asp Leu Thr Ser
 50 55 60
 Val Gln Asn Leu Leu Lys Lys His Gln Ala Phe Glu Ala Asp Ile Ala
 65 70 75 80
 Ala His Glu Xaa Asp Arg Ile Gln Ala Leu Asn Glu Phe Ala Gln Gln
 85 90 95
 Leu Ile Gln Glu Asn His Tyr Ala Ser Glu Glu
 100 105

<210> 78
 <211> 588
 <212> PRT
 <213> Homo sapiens

<400> 78
 Met Ala Arg Gly Gly Ala Gly Ala Glu Glu Ala Ser Leu Arg Ser Asn
 1 5 10 15
 Ala Leu Ser Trp Leu Ala Cys Gly Leu Leu Ala Leu Leu Ala Asn Ala
 20 25 30

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Trp	Ile	Ile	Leu	Ser	Ile	Ser	Ala	Lys	Gln	Gln	Lys	His	Lys	Pro	Leu
		35					40					45			
Glu	Leu	Leu	Leu	Cys	Phe	Leu	Ala	Gly	Thr	His	Ile	Leu	Met	Ala	Ala
	50					55					60				
Val	Pro	Leu	Thr	Thr	Phe	Ala	Val	Val	Gln	Leu	Arg	Arg	Gln	Ala	Ser
	65				70					75					80
Ser	Asp	Tyr	Asp	Trp	Asn	Glu	Ser	Ile	Cys	Lys	Val	Phe	Val	Ser	Thr
				85					90					95	
Tyr	Tyr	Thr	Leu	Ala	Leu	Ala	Thr	Cys	Phe	Thr	Val	Ala	Ser	Leu	Ser
			100					105					110		
Tyr	His	Arg	Met	Trp	Met	Val	Arg	Trp	Pro	Val	Asn	Tyr	Arg	Leu	Ser
		115					120					125			
Asn	Ala	Lys	Lys	Gln	Ala	Leu	His	Ala	Val	Met	Gly	Ile	Trp	Met	Val
	130					135					140				
Ser	Phe	Ile	Leu	Ser	Thr	Leu	Pro	Ser	Ile	Gly	Trp	His	Asn	Asn	Gly
	145				150					155					160
Glu	Arg	Tyr	Tyr	Ala	Arg	Gly	Cys	Gln	Phe	Ile	Val	Ser	Lys	Ile	Gly
				165					170					175	
Leu	Gly	Phe	Gly	Val	Cys	Phe	Ser	Leu	Leu	Leu	Leu	Gly	Gly	Ile	Val
			180					185					190		
Met	Gly	Leu	Val	Cys	Val	Ala	Ile	Thr	Phe	Tyr	Gln	Thr	Leu	Trp	Ala
		195					200					205			
Arg	Pro	Arg	Arg	Ala	Arg	Gln	Ala	Arg	Arg	Val	Gly	Gly	Gly	Gly	Gly
	210					215					220				
Thr	Lys	Ala	Gly	Gly	Pro	Gly	Ala	Leu	Gly	Thr	Arg	Pro	Ala	Phe	Glu
	225				230					235					240
Val	Pro	Ala	Ile	Val	Val	Glu	Asp	Ala	Arg	Gly	Lys	Arg	Arg	Ser	Ser
				245					250					255	
Leu	Asp	Gly	Ser	Glu	Ser	Ala	Lys	Thr	Ser	Leu	Gln	Val	Thr	Asn	Leu
			260					265					270		
Val	Ser	Ala	Ile	Val	Phe	Leu	Tyr	Asp	Ser	Leu	Thr	Gly	Val	Pro	Ile
		275					280					285			
Leu	Val	Val	Ser	Phe	Phe	Ser	Leu	Lys	Ser	Asp	Ser	Ala	Pro	Pro	Trp
	290					295					300				
Met	Val	Leu	Ala	Val	Leu	Trp	Cys	Ser	Met	Ala	Gln	Thr	Leu	Leu	Leu
	305				310					315					320
Pro	Ser	Phe	Ile	Trp	Ser	Cys	Glu	Arg	Tyr	Arg	Ala	Asp	Val	Arg	Thr
				325					330					335	
Val	Trp	Glu	Gln	Cys	Val	Ala	Ile	Met	Ser	Glu	Glu	Asp	Gly	Asp	Asp
			340					345					350		

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Asp Gly Gly Cys Asp Asp Tyr Ala Glu Gly Arg Val Cys Lys Val Arg
355 360 365

Phe Asp Ala Asn Gly Ala Thr Gly Pro Gly Ser Arg Asp Pro Ala Gln
370 375 380

Val Lys Leu Leu Pro Gly Arg His Met Leu Phe Pro Pro Leu Glu Arg
385 390 395 400

Val His Tyr Leu Gln Val Pro Leu Ser Arg Arg Leu Ser His Asp Glu
405 410 415

Thr Asn Ile Phe Ser Thr Pro Arg Glu Pro Gly Ser Phe Leu His Lys
420 425 430

Trp Ser Ser Ser Asp Asp Ile Arg Val Leu Pro Ala Gln Ser Arg Ala
435 440 445

Leu Gly Gly Pro Pro Glu Tyr Leu Gly Gln Arg His Arg Leu Glu Asp
450 455 460

Glu Glu Asp Glu Glu Glu Ala Glu Gly Gly Gly Leu Ala Ser Leu Arg
465 470 475 480

Gln Phe Leu Glu Ser Gly Val Leu Gly Ser Gly Gly Gly Pro Pro Arg
485 490 495

Gly Pro Gly Phe Phe Arg Glu Glu Ile Thr Thr Phe Ile Asp Glu Thr
500 505 510

Pro Leu Pro Ser Pro Thr Ala Ser Pro Gly His Ser Pro Arg Arg Pro
515 520 525

Arg Pro Leu Gly Leu Ser Pro Arg Arg Leu Ser Leu Gly Ser Pro Glu
530 535 540

Ser Arg Ala Val Gly Leu Pro Leu Gly Leu Ser Ala Gly Arg Arg Cys
545 550 555 560

Ser Leu Thr Gly Gly Glu Glu Ser Ala Arg Ala Trp Gly Gly Ser Trp
565 570 575

Gly Pro Gly Asn Pro Ile Phe Pro Gln Leu Thr Leu
580 585

<210> 79

<211> 227

<212> PRT

<213> Homo sapiens

<400> 79

Ile Thr Phe Tyr Gln Thr Leu Trp Ala Arg Pro Arg Arg Ala Arg Gln
1 5 10 15

Ala Arg Arg Val Gly Gly Gly Gly Gly Thr Lys Ala Gly Gly Pro Gly
20 25 30

Ala Leu Gly Thr Arg Pro Ala Phe Glu Val Pro Ala Ile Val Val Glu
35 40 45

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Asp Ala Arg Gly Lys Arg Arg Ser Ser Leu Asp Gly Ser Glu Ser Ala
 50 55 60

Lys Thr Ser Leu Gln Val Thr Asn Leu Val Val Ser Phe Phe Ser Leu
 65 70 75 80

Lys Ser Asp Ser Ala Pro Pro Trp Met Val Leu Ala Val Leu Trp Cys
 85 90 95

Ser Met Ala Gln Thr Leu Leu Leu Pro Ser Phe Ile Trp Ser Cys Glu
 100 105 110

Arg Tyr Arg Ala Asp Val Arg Thr Val Trp Glu Gln Cys Val Ala Ile
 115 120 125

Met Ser Glu Glu Asp Gly Asp Asp Asp Gly Gly Cys Asp Asp Tyr Ala
 130 135 140

Glu Gly Arg Val Cys Lys Val Arg Phe Asp Ala Asn Gly Ala Thr Gly
 145 150 155 160

Pro Gly Ser Arg Asp Pro Ala Gln Val Lys Leu Leu Pro Gly Arg His
 165 170 175

Met Leu Phe Pro Pro Leu Glu Arg Val His Tyr Leu Gln Leu Lys Lys
 180 185 190

Leu Asp Leu Ala Ala Ala Ala Ala His Thr Phe Phe Val Ala Asn Pro
 195 200 205

Met His Leu Gln Met Arg Glu Asp Met Ala Lys Tyr Arg Arg Met Ser
 210 215 220

Gly Val Arg
 225

<210> 80
 <211> 425
 <212> PRT
 <213> Homo sapiens

<400> 80

Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys
 1 5 10 15

Gly Pro Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys
 20 25 30

Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro
 35 40 45

Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser
 50 55 60

Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu
 65 70 75 80

Ala Thr Thr Gln Lys Ala Glu Lys Glu Val Thr Arg Met Val Ile Ile
245 250 255

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Met Val Ile Ala Phe Leu Ile Cys Trp Val Pro Tyr Ala Ser Val Ala
 260 265 270

Phe Tyr Ile Phe Thr His Gln Gly Ser Asn Phe Gly Pro Ile Phe Met
 275 280 285

Thr Ile Pro Ala Phe Phe Ala Lys Ser Ala Ala Ile Tyr Asn Pro Val
 290 295 300

Ile Tyr Ile Met Met Asn Lys Gln Phe Arg Asn Cys Met Leu Thr Thr
 305 310 315 320

Ile Cys Cys Gly Lys Asn Pro Leu Gly Asp Asp Glu Ala Ser Ala Thr
 325 330 335

Val Ser Lys Thr Glu Thr Ser Gln Val Ala Pro Ala
 340 345

<210> 82
 <211> 460
 <212> PRT
 <213> Rattus Norvegicus

<400> 82
 Met Asn Thr Ser Val Pro Pro Ala Val Ser Pro Asn Ile Thr Val Leu
 1 5 10 15

Ala Pro Gly Lys Gly Pro Trp Gln Val Ala Phe Ile Gly Ile Thr Thr
 20 25 30

Gly Leu Leu Ser Leu Ala Thr Val Thr Gly Asn Leu Leu Val Leu Ile
 35 40 45

Ser Phe Lys Val Asn Thr Glu Leu Lys Thr Val Asn Asn Tyr Phe Leu
 50 55 60

Leu Ser Leu Ala Cys Ala Asp Leu Ile Ile Gly Thr Phe Ser Met Asn
 65 70 75 80

Leu Tyr Thr Thr Tyr Leu Leu Met Gly His Trp Ala Leu Gly Thr Leu
 85 90 95

Ala Cys Asp Leu Trp Leu Ala Leu Asp Tyr Val Ala Ser Asn Ala Ser
 100 105 110

Val Met Asn Leu Leu Leu Ile Ser Phe Asp Arg Tyr Phe Ser Val Thr
 115 120 125

Arg Pro Leu Ser Tyr Arg Ala Lys Arg Thr Pro Arg Arg Ala Ala Leu
 130 135 140

Met Ile Gly Leu Ala Trp Leu Val Ser Phe Val Leu Trp Ala Pro Ala
 145 150 155 160

Ile Leu Phe Trp Gln Tyr Leu Val Gly Glu Arg Thr Val Leu Ala Gly
 165 170 175

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Gln	Cys	Tyr	Ile	Gln	Phe	Leu	Ser	Gln	Pro	Ile	Ile	Thr	Phe	Gly	Thr
			180					185					190		
Ala	Met	Ala	Ala	Phe	Tyr	Leu	Pro	Val	Thr	Val	Met	Cys	Thr	Leu	Tyr
		195					200					205			
Trp	Arg	Ile	Tyr	Arg	Glu	Thr	Glu	Asn	Arg	Ala	Arg	Glu	Leu	Ala	Ala
	210					215					220				
Leu	Gln	Gly	Ser	Glu	Thr	Pro	Gly	Lys	Gly	Gly	Gly	Ser	Ser	Ser	Ser
225					230					235					240
Ser	Glu	Arg	Ser	Gln	Pro	Gly	Ala	Glu	Gly	Ser	Pro	Glu	Ser	Pro	Pro
				245					250					255	
Gly	Arg	Cys	Cys	Arg	Cys	Cys	Arg	Ala	Pro	Arg	Leu	Leu	Gln	Ala	Tyr
			260					265					270		
Ser	Trp	Lys	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Gly	Ser	Met	Glu	Ser	Leu
		275					280					285			
Thr	Ser	Ser	Glu	Gly	Glu	Glu	Pro	Gly	Ser	Glu	Val	Val	Ile	Lys	Met
	290					295					300				
Pro	Met	Val	Asp	Ser	Glu	Ala	Gln	Ala	Pro	Thr	Lys	Gln	Pro	Pro	Lys
305					310					315					320
Ser	Ser	Pro	Asn	Thr	Val	Lys	Arg	Pro	Thr	Lys	Lys	Gly	Arg	Asp	Arg
				325					330					335	
Gly	Gly	Lys	Gly	Gln	Lys	Pro	Arg	Gly	Lys	Glu	Gln	Leu	Ala	Lys	Arg
			340					345					350		
Lys	Thr	Phe	Ser	Leu	Val	Lys	Glu	Lys	Lys	Ala	Ala	Arg	Thr	Leu	Ser
		355					360					365			
Ala	Ile	Leu	Leu	Ala	Phe	Ile	Leu	Thr	Trp	Thr	Pro	Tyr	Asn	Ile	Met
	370					375					380				
Val	Leu	Val	Ser	Thr	Phe	Cys	Lys	Asp	Cys	Val	Pro	Glu	Thr	Leu	Trp
385					390					395					400
Glu	Leu	Gly	Tyr	Trp	Leu	Cys	Tyr	Val	Asn	Ser	Thr	Val	Asn	Pro	Met
				405					410					415	
Cys	Tyr	Ala	Leu	Cys	Asn	Lys	Ala	Phe	Arg	Asp	Thr	Phe	Arg	Leu	Leu
			420					425					430		
Leu	Leu	Cys	Arg	Trp	Asp	Lys	Arg	Arg	Trp	Arg	Lys	Ile	Pro	Lys	Arg
		435					440					445			
Pro	Gly	Ser	Val	His	Arg	Thr	Pro	Ser	Arg	Gln	Cys				
	450					455					460				

<210> 83

<211> 350

<212> PRT

<213> Homo sapiens

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<400> 83

Met	Ser	Asn	Ile	Thr	Asp	Pro	Gln	Met	Trp	Asp	Phe	Asp	Asp	Leu	Asn
1				5					10					15	
Phe	Thr	Gly	Met	Pro	Pro	Ala	Asp	Glu	Asp	Tyr	Ser	Pro	Cys	Met	Leu
			20					25					30		
Glu	Thr	Glu	Thr	Leu	Asn	Lys	Tyr	Val	Val	Ile	Ile	Ala	Tyr	Ala	Leu
		35					40					45			
Val	Phe	Leu	Leu	Ser	Leu	Leu	Gly	Asn	Ser	Leu	Val	Met	Leu	Val	Ile
	50					55					60				
Leu	Tyr	Ser	Arg	Val	Gly	Arg	Ser	Val	Thr	Asp	Val	Tyr	Leu	Leu	Asn
65					70					75					80
Leu	Ala	Leu	Ala	Asp	Leu	Leu	Phe	Ala	Leu	Thr	Leu	Pro	Ile	Trp	Ala
				85					90					95	
Ala	Ser	Lys	Val	Asn	Gly	Trp	Ile	Phe	Gly	Thr	Phe	Leu	Cys	Lys	Val
			100					105					110		
Val	Ser	Leu	Leu	Lys	Glu	Val	Asn	Phe	Tyr	Ser	Gly	Ile	Leu	Leu	Leu
		115					120					125			
Ala	Cys	Ile	Ser	Val	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Thr	Arg
	130					135					140				
Thr	Leu	Thr	Gln	Lys	Arg	His	Leu	Val	Lys	Phe	Val	Cys	Leu	Gly	Cys
145					150					155					160
Trp	Gly	Leu	Ser	Met	Asn	Leu	Ser	Leu	Pro	Phe	Phe	Leu	Phe	Arg	Gln
				165					170					175	
Ala	Tyr	His	Pro	Asn	Asn	Ser	Ser	Pro	Val	Cys	Tyr	Glu	Val	Leu	Gly
			180					185					190		
Asn	Asp	Thr	Ala	Lys	Trp	Arg	Met	Val	Leu	Arg	Ile	Leu	Pro	His	Thr
		195					200					205			
Phe	Gly	Phe	Ile	Val	Pro	Leu	Phe	Val	Met	Leu	Phe	Cys	Tyr	Gly	Phe
	210					215					220				
Thr	Leu	Arg	Thr	Leu	Phe	Lys	Ala	His	Met	Gly	Gln	Lys	His	Arg	Ala
225					230					235					240
Met	Arg	Val	Ile	Phe	Ala	Val	Val	Leu	Ile	Phe	Leu	Leu	Cys	Trp	Leu
				245					250					255	
Pro	Tyr	Asn	Leu	Val	Leu	Leu	Ala	Asp	Thr	Leu	Met	Arg	Thr	Gln	Val
			260					265					270		
Ile	Gln	Glu	Thr	Cys	Glu	Arg	Arg	Asn	Asn	Ile	Gly	Arg	Ala	Leu	Asp
		275					280					285			
Ala	Thr	Glu	Ile	Leu	Gly	Phe	Leu	His	Ser	Cys	Leu	Asn	Pro	Ile	Ile
	290					295					300				
Tyr	Ala	Phe	Ile	Gly	Gln	Asn	Phe	Arg	His	Gly	Phe	Leu	Lys	Ile	Leu
305					310					315					320

Arg Val Leu Leu Leu Ile Ser Gly Val Trp Leu Leu Ser Leu Leu Ile
225 230 235 240

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Ser	Ser	Pro	Pro	Leu	Ile	Gly	Trp	Asn	Asp	Trp	Pro	Asp	Glu	Phe	Thr	245	250	255
Ser	Ala	Thr	Pro	Cys	Glu	Leu	Thr	Ser	Gln	Arg	Gly	Tyr	Val	Ile	Tyr	260	265	270
Ser	Ser	Leu	Gly	Ser	Phe	Phe	Ile	Pro	Leu	Ala	Ile	Met	Thr	Ile	Val	275	280	285
Tyr	Ile	Glu	Ile	Phe	Val	Ala	Thr	Arg	Arg	Arg	Leu	Arg	Glu	Arg	Ala	290	295	300
Arg	Ala	Asn	Lys	Leu	Asn	Thr	Ile	Ala	Leu	Lys	Ser	Thr	Glu	Leu	Glu	305	310	315
Pro	Met	Ala	Asn	Ser	Ser	Pro	Val	Ala	Ala	Ser	Asn	Ser	Gly	Ser	Lys	325	330	335
Ser	Arg	Leu	Leu	Ala	Ser	Trp	Leu	Cys	Cys	Gly	Arg	Asp	Arg	Ala	Gln	340	345	350
Phe	Ala	Thr	Pro	Met	Ile	Gln	Asn	Asp	Gln	Glu	Ser	Ile	Ser	Ser	Glu	355	360	365
Thr	His	Gln	Pro	Gln	Asp	Ser	Ser	Lys	Ala	Gly	Pro	His	Gly	Asn	Ser	370	375	380
Asp	Pro	Gln	Gln	Gln	His	Val	Val	Val	Leu	Val	Lys	Lys	Ser	Arg	Arg	385	390	395
Ala	Lys	Thr	Lys	Asp	Ser	Ile	Lys	His	Gly	Lys	Thr	Arg	Gly	Gly	Arg	405	410	415
Lys	Ser	Gln	Ser	Ser	Ser	Thr	Cys	Glu	Pro	His	Gly	Glu	Gln	Gln	Leu	420	425	430
Leu	Pro	Ala	Gly	Gly	Asp	Gly	Gly	Ser	Cys	Gln	Pro	Gly	Gly	Gly	His	435	440	445
Ser	Gly	Gly	Gly	Lys	Ser	Asp	Ala	Glu	Ile	Ser	Thr	Glu	Ser	Gly	Ser	450	455	460
Asp	Pro	Lys	Gly	Cys	Ile	Gln	Val	Cys	Val	Thr	Gln	Ala	Asp	Glu	Gln	465	470	475
Thr	Ser	Leu	Lys	Leu	Thr	Pro	Pro	Gln	Ser	Ser	Thr	Gly	Val	Ala	Ala	485	490	495
Val	Ser	Val	Thr	Pro	Leu	Gln	Lys	Lys	Thr	Ser	Gly	Val	Asn	Gln	Phe	500	505	510
Ile	Glu	Glu	Lys	Gln	Lys	Ile	Ser	Leu	Ser	Lys	Glu	Arg	Arg	Ala	Ala	515	520	525
Arg	Thr	Leu	Gly	Ile	Ile	Met	Gly	Val	Phe	Val	Ile	Cys	Trp	Leu	Pro	530	535	540
Phe	Phe	Leu	Met	Tyr	Val	Ile	Leu	Pro	Phe	Cys	Gln	Thr	Cys	Cys	Pro	545	550	555
																		560

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Thr Asn Lys Phe Lys Asn Phe Ile Thr Trp Leu Gly Tyr Ile Asn Ser
 565 570 575

Gly Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn Leu Asp Tyr Arg Arg
 580 585 590

Ala Phe Lys Arg Leu Leu Gly Leu Asn
 595 600

<210> 85
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 85
 agatgccacc ttccaggct 19

<210> 86
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 86
 ggagaagtgc atggccctc 19

<210> 87
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Probe

<400> 87
 tctcatcgtc tgactcctcg tcgttgg 27

<210> 88
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 88
 ggcggtgcac acagttat 18

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<210> 89
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 89
 agagagcgct ccaaatacca t

21

<210> 90
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 90
 Lys Arg Arg Ser
 1

<210> 91
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 91
 Ser Ser Ile Asp
 1

<210> 92
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 92
 Ser Arg Gln Asp
 1

<210> 93
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 93
 Gly Ser Ala Val Gly Trp
 1 5

<210> 94
 <211> 6
 <212> PRT
 <213> Homo sapiens

<400> 94
 Gly Leu Gly Phe Gly Val
 1 5

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<210> 95
<211> 6
<212> PRT
<213> Homo sapiens

<400> 95
Gly Gly Ser Val Ala Met
1 5

<210> 96
<211> 6
<212> PRT
<213> Homo sapiens

<400> 96
Gly Val Ile Cys Thr Ala
1 5

<210> 97
<211> 6
<212> PRT
<213> Homo sapiens

<400> 97
Gly Ser Glu Pro Ala Lys
1 5

<210> 98
<211> 6
<212> PRT
<213> Homo sapiens

<400> 98
Gly Leu Val Thr Thr Ile
1 5

<210> 99
<211> 4
<212> PRT
<213> Homo sapiens

<400> 99
Gln Gly Lys Arg
1

<210> 100
<211> 4
<212> PRT
<213> Homo sapiens

<400> 100
Lys Arg Arg Ser
1

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<210> 101
<211> 4
<212> PRT
<213> Homo sapiens

<400> 101
Arg Arg Phe Ser
1

<210> 102
<211> 4
<212> PRT
<213> Homo sapiens

<400> 102
Arg Arg Ala Ser
1

<210> 103
<211> 4
<212> PRT
<213> Homo sapiens

<400> 103
Arg Arg Arg Ser
1

<210> 104
<211> 4
<212> PRT
<213> Homo sapiens

<400> 104
Ser Ser Ile Asp
1

<210> 105
<211> 4
<212> PRT
<213> Homo sapiens

<400> 105
Ser Ser Asp Glu
1

<210> 106
<211> 4
<212> PRT
<213> Homo sapiens

<400> 106
Thr Ser Leu Glu
1

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<210> 107
<211> 4
<212> PRT
<213> Homo sapiens

<400> 107
Ser Ala Leu Glu
1

<210> 108
<211> 4
<212> PRT
<213> Homo sapiens

<400> 108
Ser His Asp Asp
1

<210> 109
<211> 4
<212> PRT
<213> Homo sapiens

<400> 109
Ser Gly Glu Asp
1

<210> 110
<211> 4
<212> PRT
<213> Homo sapiens

<400> 110
Ser Ala Leu Asp
1

<210> 111
<211> 4
<212> PRT
<213> Homo sapiens

<400> 111
Thr Ala Phe Glu
1

<210> 112
<211> 4
<212> PRT
<213> Homo sapiens

<400> 112
Ser Trp Gly Glu
1

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<210> 113
<211> 4
<212> PRT
<213> Homo sapiens

<400> 113
Ser Pro Ser Glu
1

<210> 114
<211> 7
<212> PRT
<213> Homo sapiens

<400> 114
Arg Ser Leu Asp Tyr Gly Tyr
1 5

<210> 115
<211> 6
<212> PRT
<213> Homo sapiens

<400> 115
Gly Ser Ala Val Gly Trp
1 5

<210> 116
<211> 6
<212> PRT
<213> Homo sapiens

<400> 116
Gly Leu Gly Phe Gly Val
1 5

<210> 117
<211> 6
<212> PRT
<213> Homo sapiens

<400> 117
Gly Gly Ser Val Ala Met
1 5

<210> 118
<211> 6
<212> PRT
<213> Homo sapiens

<400> 118
Gly Val Ile Cys Thr Ala
1 5

- 120 -

<210> 119
<211> 6
<212> PRT
<213> Homo sapiens

<400> 119
Gly Ser Glu Pro Ala Lys
1 5

<210> 120
<211> 6
<212> PRT
<213> Homo sapiens

<400> 120
Gly Leu Val Thr Thr Ile
1 5

<210> 121
<211> 6
<212> PRT
<213> Homo sapiens

<400> 121
Gly Ala Asp Pro Gly Glu
1 5

<210> 122
<211> 6
<212> PRT
<213> Homo sapiens

<400> 122
Gly Leu Ser Ala Ser Trp
1 5

<210> 123
<211> 6
<212> PRT
<213> Homo sapiens

<400> 123
Gly Gly Leu Arg Ala Ala
1 5

<210> 124
<211> 6
<212> PRT
<213> Homo sapiens

<400> 124
Gly Gly Gly Gly Ser Thr
1 5

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<210> 125
 <211> 4
 <212> PRT
 <213> Homo sapiens

<400> 125
 Gln Gly Lys Arg
 1

<210> 126
 <211> 458
 <212> PRT
 <213> Mus Musculus

<400> 126
 Met Thr Lys Glu Met Thr Glu Asn Gln Arg Leu Cys Pro His Glu Arg
 1 5 10 15
 Glu Asp Ala Asp Cys Ser Ser Glu Ser Val Lys Phe Asp Ala Arg Ser
 20 25 30
 Met Thr Ala Ser Leu Pro His Ser Thr Lys Asn Gly Pro Ser Val Gln
 35 40 45
 Glu Lys Leu Lys Ser Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu
 50 55 60
 Val Phe Ala Val Leu Ile Pro Val Val Gly Ile Val Thr Ala Gln Leu
 65 70 75 80
 Leu Asn Trp Glu Met Lys Asn Cys Leu Val Cys Ser Arg Asn Thr Ser
 85 90 95
 Asp Thr Ser Gln Gly Pro Met Glu Lys Glu Asn Thr Ser Asn Val Glu
 100 105 110
 Met Arg Phe Thr Ile Ile Met Ala His Met Lys Asp Met Glu Glu Arg
 115 120 125
 Ile Gln Ser Ile Ser Asn Ser Lys Ala Asp Leu Ile Asp Thr Gly Arg
 130 135 140
 Phe Gln Asn Phe Ser Met Ala Thr Asp Gln Arg Leu Asn Asp Ile Leu
 145 150 155 160
 Leu Gln Leu Asn Ser Leu Ile Leu Ser Val Gln Glu His Gly Asn Ser
 165 170 175
 Leu Asp Ala Ile Ser Lys Ser Leu Gln Ser Leu Asn Met Thr Leu Leu
 180 185 190
 Asp Val Gln Leu His Thr Glu Thr Leu His Val Arg Val Arg Glu Ser
 195 200 205
 Thr Ala Lys Gln Gln Glu Asp Ile Ser Lys Leu Glu Glu Arg Val Tyr
 210 215 220

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Lys Val Ser Ala Glu Val Gln Ser Val Lys Glu Glu Gln Ala His Val
 225 230 235 240
 Glu Gln Glu Val Lys Gln Glu Val Arg Val Leu Asn Asn Ile Thr Asn
 245 250 255
 Asp Leu Arg Leu Lys Asp Trp Glu His Ser Gln Thr Leu Lys Asn Ile
 260 265 270
 Thr Phe Ile Gln Gly Pro Pro Gly Pro Gln Gly Glu Lys Gly Asp Arg
 275 280 285
 Gly Leu Thr Gly Gln Thr Gly Pro Pro Gly Ala Pro Gly Ile Arg Gly
 290 295 300
 Ile Pro Gly Val Lys Gly Asp Arg Gly Gln Ile Gly Phe Pro Gly Gly
 305 310 315 320
 Arg Gly Asn Pro Gly Ala Pro Gly Lys Pro Gly Arg Ser Gly Ser Pro
 325 330 335
 Gly Pro Lys Gly Gln Lys Gly Glu Lys Gly Ser Val Gly Gly Ser Thr
 340 345 350
 Pro Leu Lys Thr Val Arg Leu Val Gly Gly Ser Gly Ala His Glu Gly
 355 360 365
 Arg Val Glu Ile Phe His Gln Gly Gln Trp Gly Thr Ile Cys Asp Asp
 370 375 380
 Arg Trp Asp Ile Arg Ala Gly Gln Val Val Cys Arg Ser Leu Gly Tyr
 385 390 395 400
 Gln Glu Val Leu Ala Val His Lys Arg Ala His Phe Gly Gln Gly Thr
 405 410 415
 Gly Pro Ile Trp Leu Asn Glu Val Met Cys Phe Gly Arg Glu Ser Ser
 420 425 430
 Ile Glu Asn Cys Lys Ile Asn Gln Trp Gly Val Leu Ser Cys Ser His
 435 440 445
 Ser Glu Asp Ala Gly Val Thr Cys Thr Ser
 450 455

<210> 127

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Xaa at position 2 and 4 may be any amino acid
 except Pro

<220>

<223> Xaa at position 3 may be Ser or Thr

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<220>

<223> Description of Artificial Sequence: Amidation
consensus site

<400> 127

Asn Xaa Xaa Xaa
1

<210> 128

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<220>

<223> Xaa at position 2 can be between 4 and 14 amino
acids

<220>

<223> Xaa at position, if present, may be between 0 or 2
amino acids

<220>

<223> Xaa at position 6 may be between 2 and 4 amino
acids

<220>

<223> Xaa at position 8 may be between 6 and 12 amino
acids

<220>

<223> Xaa at position 10 may be between 6 and 10 amino
acids

<400> 128

Cys Xaa Cys Xaa Cys Xaa Cys Xaa Cys Xaa Cys
1 5 10

<210> 129

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

<220>

<223> Xaa at position 2 may be 4 or 6 amino acids

<220>

<223> Xaa at position 6 may be 5 or 10 amino acids

<220>

<223> Xaa at position 8 may be 0 or 2 amino acids

- 124 -

<220>

<223> Xaa at position 10 may be 7 or 11 amino acids

<220>

<223> Xaa at position 12 may be 4 or 6 amino acids

<400> 129

Cys	Xaa	Phe	Tyr	His	Xaa	Cys	Xaa	Cys	Xaa	Cys	Xaa	Asp	Asn	Glu	Gln
1				5				10						15	

Ser	Lys	Pro	Xaa	Xaa	Cys
			20		

<210> 130

<211> 39

<212> PRT

<213> Mus musculus

<400> 130

Cys	Arg	Gln	Gln	Glu	Phe	Lys	Asp	Arg	Ser	Gly	Asn	Cys	Val	Leu	Cys
1				5					10					15	

Lys	Gln	Cys	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe	Gly
			20					25					30		

Tyr	Gly	Glu	Asp	Ala	Gln	Cys
						35

<210> 131

<211> 40

<212> PRT

<213> Mus musculus

<400> 131

Cys	Arg	Pro	His	Arg	Phe	Lys	Glu	Asp	Trp	Gly	Phe	Gln	Lys	Cys	Lys
1				5					10					15	

Pro	Cys	Ala	Asp	Cys	Ala	Leu	Val	Asn	Arg	Phe	Gln	Arg	Ala	Asn	Cys
			20					25					30		

Ser	His	Thr	Ser	Asp	Ala	Val	Cys
							40

<210> 132

<211> 39

<212> PRT

<213> Mus musculus

<400> 132

Cys	Arg	Gln	Gln	Glu	Phe	Lys	Asp	Arg	Ser	Gly	Asn	Cys	Val	Leu	Cys
1				5					10					15	

Lys	Gln	Cys	Gly	Pro	Gly	Met	Glu	Leu	Ser	Lys	Glu	Cys	Gly	Phe	Gly
			20					25					30		

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Tyr Gly Glu Asp Ala Gln Cys
35

<210> 133
<211> 40
<212> PRT
<213> Mus musculus

<400> 133
Cys Arg Pro His Arg Phe Lys Glu Asp Trp Gly Phe Gln Lys Cys Lys
1 5 10 15

Pro Cys Ala Asp Cys Ala Leu Val Asn Arg Phe Gln Arg Ala Asn Cys
20 25 30

Ser His Thr Ser Asp Ala Val Cys
35 40

<210> 134
<211> 29
<212> PRT
<213> Mus musculus

<400> 134
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
1 5 10 15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys
20 25

<210> 135
<211> 29
<212> PRT
<213> Mus musculus

<400> 135
Met Ala Leu Lys Val Leu Pro Leu His Arg Thr Val Leu Phe Ala Ala
1 5 10 15

Ile Leu Phe Leu Leu His Leu Ala Cys Lys Val Ser Cys
20 25

<210> 136
<211> 25
<212> PRT
<213> Mus musculus

<400> 136
Ala Leu Ala Ala Val Ile Cys Ser Ala Leu Ala Thr Val Leu Leu Ala
1 5 10 15

Leu Leu Ile Leu Cys Val Ile Tyr Cys
20 25

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<210> 137
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 137
 Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val Phe Val Val Ser Leu
 1 5 10 15
 Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile Leu Lys Met Lys
 20 25 30

<210> 138
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 138
 Phe Ser Met Leu Ala Ala Tyr Met Phe Leu Leu Ile Val Leu Gly Phe
 1 5 10 15
 Pro Ile Asn Phe Leu Thr Leu Tyr Val Thr Val Gln His Lys Lys
 20 25 30

<210> 139
 <211> 31
 <212> PRT
 <213> Rattus Norvegicus

<400> 139
 Val Ala Phe Ile Gly Ile Thr Thr Gly Leu Leu Ser Leu Ala Thr Val
 1 5 10 15
 Thr Gly Asn Leu Leu Val Leu Ile Ser Phe Lys Val Asn Thr Glu
 20 25 30

<210> 140
 <211> 31
 <212> PRT
 <213> Homo sapiens

<400> 140
 Lys Tyr Val Val Ile Ile Ala Tyr Ala Leu Val Phe Leu Leu Ser Leu
 1 5 10 15
 Leu Gly Asn Ser Leu Val Met Leu Val Ile Leu Tyr Ser Arg Val
 20 25 30

<210> 141
 <211> 31
 <212> PRT
 <213> Drosophila melanogaster

<400> 141
 Ala Leu Leu Thr Ala Leu Val Leu Ser Val Ile Ile Val Leu Thr Ile
 1 5 10 15

Ile Gly Asn Ile Leu Val Ile Leu Ser Val Phe Thr Tyr Lys Pro
20 25 30

```
<210> 142
<211> 28
<212> PRT
<213> Homo sapiens
```

```
<400> 142
Val Val Tyr Met Leu His Leu Ala Thr Ala Asp Val Leu Phe Val Ser
  1             5             10             15
```

Val Leu Pro Phe Lys Ile Ser Tyr Tyr Phe Ser Gly
20 25

```
<210> 143
<211> 28
<212> PRT
<213> Homo sapiens
```

```
<400> 143
Asn Tyr Ile Leu Leu Asn Leu Ala Val Ala Asp Leu Phe Met Val Leu
  1             5             10            15
```

Gly Gly Phe Thr Ser Thr Leu Tyr Thr Ser Leu His
20 25

```
<210> 144
<211> 28
<212> PRT
<213> Rattus Norvegicus
```

```
<400> 144
Asn Tyr Phe Leu Leu Ser Leu Ala Cys Ala Asp Leu Ile Ile Gly Thr
  1             5             10             15
```

Phe Ser Met Asn Leu Tyr Thr Thr Tyr Leu Leu Met
20 25

```
<210> 145
<211> 28
<212> PRT
<213> Homo sapiens
```

```
<400> 145
Asp Val Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu
  1             5             10            15
```

Thr Leu Pro Ile Trp Ala Ala Ser Lys Val Asn Gly
20 25

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<210> 146
 <211> 28
 <212> PRT
 <213> Drosophila melanogaster

<400> 146
 Asn Phe Phe Ile Val Ser Leu Ala Val Ala Asp Leu Thr Val Ala Leu
 1 5 10 15
 Leu Val Leu Pro Phe Asn Val Ala Tyr Ser Ile Leu
 20 25

<210> 147
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 147
 Arg Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu
 1 5 10 15
 Leu Met Thr Val Ile Ser Ile Asp Arg
 20 25

<210> 148
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 148
 Asn Leu Glu Gly Phe Phe Ala Thr Leu Gly Gly Glu Ile Ala Leu Trp
 1 5 10 15
 Ser Leu Val Val Leu Ala Ile Glu Arg
 20 25

<210> 149
 <211> 25
 <212> PRT
 <213> Rattus Norvegicus

<400> 149
 Asp Leu Trp Leu Ala Leu Asp Tyr Val Ala Ser Asn Ala Ser Val Met
 1 5 10 15
 Asn Leu Leu Leu Ile Ser Phe Asp Arg
 20 25

<210> 150
 <211> 25
 <212> PRT
 <213> Homo sapiens

<400> 150
 Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly Ile Leu
 1 5 10 15

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Leu Leu Ala Cys Ile Ser Val Asp Arg
20 25

<210> 151
<211> 25
<212> PRT
<213> Drosophila melanogaster

<400> 151
Lys Leu Trp Leu Thr Cys Asp Val Leu Cys Cys Thr Ser Ser Ile Leu
1 5 10 15

Asn Leu Cys Ala Ile Ala Leu Asp Arg
20 25

<210> 152
<211> 27
<212> PRT
<213> Homo sapiens

<400> 152
Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu Ala Ile Trp Ala Leu Ala
1 5 10 15

Ile Ala Gly Val Val Pro Leu Val Leu Lys Glu
20 25

<210> 153
<211> 27
<212> PRT
<213> Homo sapiens

<400> 153
Gly Glu Asn His Ala Ile Met Gly Val Ala Phe Thr Trp Val Met Ala
1 5 10 15

Leu Ala Cys Ala Ala Pro Pro Leu Ala Gly Trp
20 25

<210> 154
<211> 27
<212> PRT
<213> Rattus Norvegicus

<400> 154
Thr Pro Arg Arg Ala Ala Leu Met Ile Gly Leu Ala Trp Leu Val Ser
1 5 10 15

Phe Val Leu Trp Ala Pro Ala Ile Leu Phe Trp
20 25

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<210> 155
<211> 27
<212> PRT
<213> Homo sapiens

<400> 155
Lys Arg His Leu Val Lys Phe Val Cys Leu Gly Cys Trp Gly Leu Ser
1 5 10 15
Met Asn Leu Ser Leu Pro Phe Phe Leu Phe Arg
20 25

<210> 156
<211> 27
<212> PRT
<213> Drosophila melanogaster

<400> 156
Thr Val Gly Arg Val Leu Leu Leu Ile Ser Gly Val Trp Leu Leu Ser
1 5 10 15
Leu Leu Ile Ser Ser Pro Pro Leu Ile Gly Trp
20 25

<210> 157
<211> 29
<212> PRT
<213> Homo sapiens

<400> 157
Ala Tyr Tyr Phe Ser Ala Phe Ser Ala Val Phe Phe Phe Val Pro Leu
1 5 10 15
Ile Ile Ser Thr Val Cys Tyr Val Ser Ile Ile Arg Cys
20 25

<210> 158
<211> 29
<212> PRT
<213> Homo sapiens

<400> 158
Glu Ser Phe Val Ile Tyr Met Phe Val Val His Phe Thr Ile Pro Met
1 5 10 15
Ile Ile Ile Phe Phe Cys Tyr Gly Gln Leu Val Phe Thr
20 25

<210> 159
<211> 29
<212> PRT
<213> Rattus Norvegicus

<400> 159
Pro Ile Ile Thr Phe Gly Thr Ala Met Ala Ala Phe Tyr Leu Pro Val
1 5 10 15

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Thr Val Met Cys Thr Leu Tyr Trp Arg Ile Tyr Arg Glu
20 25

<210> 160
<211> 29
<212> PRT
<213> Homo sapiens

<400> 160
Met Val Leu Arg Ile Leu Pro His Thr Phe Gly Phe Ile Val Pro Leu
1 5 10 15

Phe Val Met Leu Phe Cys Tyr Gly Phe Thr Leu Arg Thr
20 25

<210> 161
<211> 29
<212> PRT
<213> Drosophila melanogaster

<400> 161
Arg Gly Tyr Val Ile Tyr Ser Ser Leu Gly Ser Phe Phe Ile Pro Leu
1 5 10 15

Ala Ile Met Thr Ile Val Tyr Ile Glu Ile Phe Val Ala
20 25

<210> 162
<211> 28
<212> PRT
<213> Homo sapiens

<400> 162
Phe Leu Ser Ala Ala Val Phe Cys Ile Phe Ile Ile Cys Phe Gly Pro
1 5 10 15

Thr Asn Val Leu Leu Ile Ala His Tyr Ser Phe Leu
20 25

<210> 163
<211> 28
<212> PRT
<213> Homo sapiens

<400> 163
Arg Met Val Ile Ile Met Val Ile Ala Phe Leu Ile Cys Trp Val Pro
1 5 10 15

Tyr Ala Ser Val Ala Phe Tyr Ile Phe Thr His Gln
20 25

- 132 -

<210> 164
 <211> 28
 <212> PRT
 <213> Rattus Norvegicus

<400> 164
 Arg Thr Leu Ser Ala Ile Leu Leu Ala Phe Ile Leu Thr Trp Thr Pro
 1 5 10 15
 Tyr Asn Ile Met Val Leu Val Ser Thr Phe Cys Lys
 20 25

<210> 165
 <211> 28
 <212> PRT
 <213> Homo sapiens

<400> 165
 Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu Leu Cys Trp Leu Pro
 1 5 10 15
 Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met Arg
 20 25

<210> 166
 <211> 28
 <212> PRT
 <213> Drosophila melanogaster

<400> 166
 Arg Thr Leu Gly Ile Ile Met Gly Val Phe Val Ile Cys Trp Leu Pro
 1 5 10 15
 Phe Phe Leu Met Tyr Val Ile Leu Pro Phe Cys Gln
 20 25

<210> 167
 <211> 33
 <212> PRT
 <213> Homo sapiens

<400> 167
 Glu Ala Ala Tyr Phe Ala Tyr Leu Leu Cys Val Cys Val Ser Ser Ile
 1 5 10 15
 Ser Ser Cys Ile Asp Pro Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys
 20 25 30

Gln

<210> 168
 <211> 33
 <212> PRT
 <213> Homo sapiens

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<400> 168

Asn	Phe	Gly	Pro	Ile	Phe	Met	Thr	Ile	Pro	Ala	Phe	Phe	Ala	Lys	Ser
1				5					10					15	

Ala	Ala	Ile	Tyr	Asn	Pro	Val	Ile	Tyr	Ile	Met	Met	Asn	Lys	Gln	Phe
			20					25					30		

Arg

<210> 169

<211> 33

<212> PRT

<213> Rattus Norvegicus

<400> 169

Cys	Val	Pro	Glu	Thr	Leu	Trp	Glu	Leu	Gly	Tyr	Trp	Leu	Cys	Tyr	Val
1				5					10					15	

Asn	Ser	Thr	Val	Asn	Pro	Met	Cys	Tyr	Ala	Leu	Cys	Asn	Lys	Ala	Phe
			20					25					30		

Arg

<210> 170

<211> 33

<212> PRT

<213> Homo sapiens

<400> 170

Asn	Asn	Ile	Gly	Arg	Ala	Leu	Asp	Ala	Thr	Glu	Ile	Leu	Gly	Phe	Leu
1				5					10					15	

His	Ser	Cys	Leu	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Ile	Gly	Gln	Asn	Phe
			20					25					30		

Arg

<210> 171

<211> 33

<212> PRT

<213> Drosophila melanogaster

<400> 171

Cys	Pro	Thr	Asn	Lys	Phe	Lys	Asn	Phe	Ile	Thr	Trp	Leu	Gly	Tyr	Ile
1				5					10					15	

Asn	Ser	Gly	Leu	Asn	Pro	Val	Ile	Tyr	Thr	Ile	Phe	Asn	Leu	Asp	Tyr
			20					25					30		

Arg

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<210> 172
 <211> 174
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: 7
 transmembrane receptor consensus sequence

<400> 172
 Gly Asn Ile Leu Val Ile Trp Val Ile Cys Arg Tyr Arg Arg Met Arg
 1 5 10 15
 Thr Pro Met Asn Tyr Phe Ile Val Asn Leu Ala Val Ala Asp Leu Leu
 20 25 30
 Phe Ser Leu Phe Thr Met Pro Phe Trp Met Val Tyr Tyr Val Met Gln
 35 40 45
 Gly Arg Trp Pro Phe Gly Asp Phe Met Cys Arg Ile Trp Met Tyr Phe
 50 55 60
 Asp Tyr Met Asn Met Tyr Ala Ser Ile Phe Phe Leu Thr Cys Ile Ser
 65 70 75 80
 Ile Asp Arg Tyr Leu Trp Ala Ile Cys His Pro Met Arg Tyr Met Arg
 85 90 95
 Trp Met Thr Pro Arg His Arg Ala Trp Val Met Ile Ile Ile Ile Trp
 100 105 110
 Val Met Ser Phe Leu Ile Ser Met Pro Pro Phe Leu Met Phe Arg Trp
 115 120 125
 Ser Thr Tyr Arg Asp Glu Asn Glu Trp Asn Met Thr Trp Cys Met Ile
 130 135 140
 Tyr Asp Trp Pro Glu Trp Met Trp Arg Trp Tyr Val Ile Leu Met Thr
 145 150 155 160
 Ile Ile Met Gly Phe Tyr Ile Pro Met Ile Ile Met Leu Phe
 165 170

<210> 173
 <211> 168
 <212> PRT
 <213> Homo sapiens

<400> 173
 Ala Asn Ala Trp Gly Ile Leu Ser Val Gly Ala Lys Gln Lys Lys Trp
 1 5 10 15
 Lys Pro Leu Glu Phe Leu Leu Cys Thr Leu Ala Ala Thr His Met Leu
 20 25 30
 Asn Val Ala Val Pro Ile Ala Thr Tyr Ser Val Val Gln Leu Arg Arg
 35 40 45

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Gln Arg Pro Asp Phe Glu Trp Asn Glu Gly Leu Cys Lys Val Phe Val
 50 55 60

Ser Thr Phe Tyr Thr Leu Thr Leu Ala Thr Cys Phe Ser Val Thr Ser
 65 70 75 80

Leu Ser Tyr His Arg Met Trp Met Val Cys Trp Pro Val Asn Tyr Arg
 85 90 95

Leu Ser Asn Ala Lys Lys Gln Ala Val His Thr Val Met Gly Ile Trp
 100 105 110

Met Val Ser Phe Ile Leu Ser Ala Leu Pro Ala Val Gly Trp His Asp
 115 120 125

Thr Ser Glu Arg Phe Tyr Thr His Gly Cys Arg Phe Ile Val Ala Glu
 130 135 140

Ile Gly Leu Gly Phe Gly Val Cys Phe Leu Leu Leu Val Gly Gly Ser
 145 150 155 160

Val Ala Met Gly Val Ile Cys Thr
 165

<210> 174

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
 sequence

<400> 174

Ile Gln Glu Arg Met Asn Glu Leu Asn Asp Arg Trp Glu Arg Leu Lys
 1 5 10 15

Glu Leu Met Glu Gln Arg Arg Gln Met Leu Glu Asp Ser Met Arg Leu
 20 25 30

Gln Gln Phe Phe Arg Asp Met Asp Glu Glu Glu Ser Trp Ile Asn Glu
 35 40 45

Lys Glu Gln Ile Leu Asn Ser Asp Asp Tyr Gly Lys Asp Leu Thr Ser
 50 55 60

Val Gln Asn Leu Leu Lys Lys His Gln Ala Phe Glu Ala Asp Ile Ala
 65 70 75 80

Ala His Glu Asp Arg Ile Gln Ala Leu Asn Glu Phe Ala Gln Gln Leu
 85 90 95

Ile Gln Glu Asn His Tyr Ala Ser Glu Glu
 100 105

- 136 -

<210> 175
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 175
 Phe Ser Ser Leu Arg Ala Asp Ala Ser Ala Pro Trp Met Ala Leu Cys
 1 5 10 15
 Val Leu Trp Cys Ser Val Ala Gln Ala Leu Leu Leu Pro Val Phe Leu
 20 25 30
 Trp Ala Cys Asp Arg Tyr Arg Ala Asp Leu Lys Ala Val Arg Glu Lys
 35 40 45
 Cys Met Ala Leu Met Ala Asn Asp Glu Glu Ser Asp Asp Glu Thr Ser
 50 55 60
 Leu Glu Gly Gly Ile Ser Pro Asp Leu Val Leu Glu Arg Ser Leu Asp
 65 70 75 80
 Tyr Gly Tyr Gly Gly Asp Phe Val Ala Leu Asp Arg Met Ala Lys Tyr
 85 90 95
 Glu Ile Ser Ala Leu Glu Gly Gly Leu Pro Gln
 100 105

<210> 176
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Xaa at position 2 may be any amino acide except:
 Glu, Asp, Arg, Lys, His, Phe, Pro, Tyr, or Trp

<220>
 <223> Xaa at position 5 may be ser, Thr, Ala, Gly, Cys
 or Asn

<220>
 <223> Xaa at position 6 may be any amino acid except Pro

<220>
 <223> Description of Artificial Sequence: Amidation
 consensus site

<400> 176
 Gly Xaa Xaa Xaa Xaa Xaa
 1 5